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Green fluorescent protein; GPP; jellyfish; marker protein; reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green fluorescent protein mutant, F64L-S175G-B222G-GPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA25195 standard; protein; 238 AA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ada25195 Green flu	Ada25221 Green flu	Green	Green	Ada25222 Green flu	7	Green	Green	Green	4	Abr44424 F64L-Y66H	_					Aaw76106 A. victor		Aaw05304 Green flu	Aeo	Ä			Aab73552 Wild-type	Aae16038 Aequorea
SUMMARIES	Ω	ADA25195	ADA25221	ADA25216	ADA25218	ADA25222	AAE16087	ADA25215	ADA25223	ADA25196	ADA25214	ABR44424	ADA25212	ADA25220	ABG32368	AAE34996	ADA25219	AAW76106	AAE16073	AAW05304	AAW24232	AAW76105	AAW40479	AAW76371	AAB73552	AAE16038
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ABG32365	ABG75980	AAE34999	AAE34985	ABR44423	ADA25217	ADA25194	ADF70380	ADM78505	ADM78577	ADQ59552	AAW65084	ABG32367	ABR44425	AAW221:01	AAW76111	AAW76110	AAW76109	AAW65079	A DWG S O 7 B	
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## ALIGNMENTS

(first entry)

The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid substitution at either proistion 65 Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein. /note= "Gly replaces wild-type Ser" Misc-difference 222 /note= "Gly replaces wild-type Glu" 'note= "Leu replaces wild-type Phe" ï Thomas (AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD. (AMSH ) AMERSHAM BIOSCIENCES UK LTD. Michael NP, Location/Qualifiers Claim 8; Fig 3; 52pp; English. 28-SEP-2001; 2001GB-00023288. 23-APR-2001; 2001GB-00009858 Jones AE, WPI; 2003-095652/09. Synthetic. Aequorea victoria. Misc-difference SLJ, GB2374868-A. 30-OCT-2002. Stubbs CCCX2X4444X4X4X4X4X4X4X4X444444444X8XXX4X4X4X4X4X4X4X4X

(AMSH ) AMERSHAM BIOSCIENCES UK LTD

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or 222. The mutants of the invention are particularly F641-S175G-E222G-GPP (ADA25196). GPP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologue cells at temperatures above 30 degrees celsius, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased sensitivity relative to wild type GFP. The GFP mutants of the invention of protein labels in living and fixed cells, as markers in cell or organelle fusion, for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein to a specific organelle, as secretion markers, as genetic reporters to be cused in combination with fluorescent activated cell sorting (FACS), as real-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents the specifically claimed Aequorea victoria GFP mutant F64L-S175G-E222G-GFP.
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Aequorea victoria.
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The invention relates to Aequorea victoria green fluorescent protein

(GFP) mutants containing an amino acid subsitution at positions 64 and

(175, and additionally an amino acid subsitution at either profistion 65

cr 222. The mutants of the invention are particularly F64L-S175G-S22G-GFP (ADA25196). GFP mutants of the

cr 222. The mutants of the invention are particularly F64L-S175G-S22G-GFP (ADA25196). GFP mutants of the

cr 222. The mutants of the invention are particularly F64L-S175G-GFP (ADA25196). GFP mutants of the

cr 222. The mon-homologous cells respective to wild type GFP when

cr 222. The mon-homologous cells at temperatures above 30 degrees

celsius, and excited at 490 nm. The mutants can also be detected in

commandian cells at lower levels of expression and with increased

celsius, and excited at 490 nm. The mutants can also be detected in

commandian cells at lower levels of expression and with increased

celsius, and excited markers for selection of transfected cells, as

protein labels in living and fixed cells, as markers in cell or organelle

cr 222 mutants of the invention of intraccellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein

cr 222. The mutants of the mutants of the invention of protein for organelle or organelle

cr 222. The mutants of the invention of intraccellular proteins to a specific organelle or organelle

cr 222. The mutants of the mutants of protein transfected cells or organelle

cr 222. The mutants of the mutants of protein to a specific organelle or organelle

cr 222. The mutants or protein and gene expression in transgenic animals, as cell or organelle
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                                                                                                                                                                                  Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
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99.6%; Pred. No. 1.3e-124;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                 Example 2; Page; 52pp; English.
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238

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ADA25218 standard, protein; 238

ADA25216

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Green fluorescent protein; GPP; jellyfish; marker protein;

reporter protein; mutant; mutein.

Green fluorescent protein mutant, F64L-S175G-GFP.

(first entry)

20-NOV-2003

ADA25218;

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The invention relates to Aequorea victoria green fluorescent protein (GPP) mutants containing an amino acid subsitution at positions 64 and 202 (GPP) mutants containing an amino acid subsitution at either prolation 65 or 222. The mutants of the invention are particularly F64L-S175G-E222G-GPP (ADA25195). GFP mutants of the invention are particularly F64L-S175G-E222G-GPP (ADA25196). GFP mutants of the carporatures above 30 degrees caption ochid expices of an non-homologous colls at temperatures above 30 degrees celsius, and excited at 490 nm. The mutants can also be detected in ammalian cells at lower levels of expression and with increased sensitivity relative to wild type GPP. The GPP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle fusion, for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein and specific organelle and markers in markers and markers and markers and markers or protein and specific organelle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
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                                                                                                                                                                                              note= "Leu replaces wild-type Phe"
                                                                                                                                                                                                                                                                          /note= "Gly replaces wild-type Glu"
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Pred. No. 2.1e-124;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michael NP,
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                                                                                                             Location/Qualifiers
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Best Local Similarity 99.6%;
Matches 237; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2001; 2001GB-00023288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-2001; 2001GB-00009858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stubbs SLJ, Jones AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-095652/09.
                                                                                                                                                                                                                                        Misc-difference 222
Synthetic.
Aequorea victoria.
                                                                                                                                                        Misc-difference 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADA25193.
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                                                                                                                                                                                                                                                                                                                                                                   GB2374868-A
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The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid substitution at positions 64 and (GFP) mutants containing an amino acid substitution at protein 65 and additionally an amino acid substitution at proteins 64 and (175, and additionally an amino acid substitution at protein 65 cor 222. The mutants of the invention are particularly F64L-S175G-E22G-CG GFP (ADA25195) or F64L-S67T-S175G-GFP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when corresponding and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased containty relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers of selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle correction for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters to be consoning to companie of the invescent activated cell sorting (FACS), as created in combination with fluorescent activated cell sorting (FACS), as creation. The present sequence represents and as reporters for bacterial companies to protein and example of the invention. Note: The present sequence is mutant used in an example of the information given on page 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                        'note= "Leu replaces wild-type Phe"
                                                                                                                                                                                                                                                                                                             /note= "Gly replaces wild-type Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2001; 2001GB-00009858.
                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2001; 2001GB-00023288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stubbs SLJ, Jones AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-095652/09.
                                                                                                                                                                                                                                                                                           Misc-difference 175
                                                                                                                                                                                 Synthetic.
Aequorea victoria.
                                                                                                                                                                                                                                                       Misc-difference 64
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VITLSYGVOCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 

1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60

MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

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                                                                                                                       VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                            61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                      NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                                     181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                     Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid substitution at either proistion 65 or 222. The mutants of the invention are particularly F64L-S175G-E222G-
                                                                       1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                      Gaps
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                           Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                          GFP; jellyfish; marker protein;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                Green fluorescent protein mutant, V163A-S175G-E222G-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Ala replaces wild-type Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Gly replaces wild-type Glu"
                                                      ;
                        Score 1268; DB 6;
Pred. No. 3.4e-124;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Gly replaces"
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BIOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                          ADA25222 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein; GFP; j reporter protein; mutant; mutein.
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                         99.4%;
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-095652/09.
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea victoria.
 Sequence 238 AA;
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(AMSH ) AMERSHAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                237;
                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB2374868-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                       121
                        Query Match
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CC GFP (ADA25195) or E64L-865T-S175G-GPP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when copressed in non-homologous cells at temperatures above 30 degrees C celsius, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased commandian cells at lower levels of expression and with increased commandian cells at lower levels of expression and with increased commandian cells at lower levels of expression and with increased commandian cells as non-toxic markers for selection of transfected cells, as sensitivity relataistic markers for selection of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein capering commandian dene expression in transgenic animals, as cell or companination with fluorescent activated cell sorting (FACS), as consentle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as cal-time probes working at near physiological concentrations, for cal-time probes working at near physiological concentrations, for detection. The present sequence represents an Aequorea victoria GFP concentrations in the specification, but is derived from the wild-type GFP concentration in the specification, but is derived from the wild-type GFP concentration in the specification, but is derived from the wild-type GFP concentration in the specification, but is derived from the wild-type GFP concentration in the specification, but is derived from the wild-type GFP concentration in the specification, but is derived from the wild-type GFP concentration in the specification of the information of the informa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VITESYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERIIFPKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGBGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 1268; DB 6;
99.2%; Pred. No. 3.4e-124;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequorea victoria GFP mutant protein (E222G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE16087 standard; protein; 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.2
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238 AA;
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Green fluorescent protein mutant, B222G-GPP

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The patent discloses functional engineered fluorescent protein and its corresponding polynucleotide. The amino acid sequence of the engineered protein is identical to Aequorea green fluorescent protein (GFP). The engineered fluorescent proteins of the invention have varied fluorescent proteins of the invention have varied fluorescent proteins change in fluorescent characteristics. They are useful a markers for change in fluorescent characteristics. They are useful as markers for protein localisation within living cells. The engineered fluorescent proteins are particularly useful for coupling engineered fluorescent proteins are particularly useful for coupling engineered fluorescent proteins to antibodies, nucleic acids or other receptors for use in detecting induction of transcription and for the simultaneous measurement of two or more processes within cells. Proteins of the invention are also useful as fluorescent energy donors or acceptors as well as biosensors of the detecting anions. They are also useful in fluorescence resonance energy transfer (FRET). The crystal structure of the GFP is useful for designing mutants having altered fluorescent characteristics which are fluorescent properties of the protein. The crystal structure of the GFP is also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit and a subsection. The crystal structure of the GFP is also and a subsection and anion bidding mit also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit also useful for designing mutants having altered anion bidding mit and a subsection and anion bidding mit and a subsection and anion bidding mit anion bidding mit and a subsection and anion bidding mit and a subs
                                                                                                                                                                                                                                                                                                                                                                                                                           New long wavelength engineered fluorescent proteins, useful as markers for gene expression, tracers of cell lineage or as fusion tags to monitor protein localization, or in detection assays, e.g. immunoassays or hybridization assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characteristics which are particularly useful for identifying amino acids whose substitution alters the specificity and affinity of the binding site to various anions, and for monitoring anion binding and therefore the concentration of the anion. The present sequence is Aequorea victoria GFP mutant protein (B222G). Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild type green fluorescent protein shown in figure 3 of the specification (AAB16038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example, Page, 181pp, English.
(UYOR-) UNIV OREGON STATE
                                                                                                                                                         Wachter R, Remington SJ;
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VTTLSYGVQCPSRYPDHMKRHDFPKSAMPEGYVQERTIFPKDDGNYKTRAEVKFEGDTLV 120 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 9 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 1 MSKGEBLFTGVVPILVBLDGDVNGHKFSVSGBGEGDATYGKLTLKFICTTGKLPVPWPTL Gaps ö 99.2%; Score 1266; DB 5; Length 238; 99.2%; Pred. No. 5.5e-124; ive 0; Mismatches 2; Indels Best Local Similarity 99.2 Matches 236; Conservative 61 121 181 61 Query Match RESULT 7 ADA25215

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Sequence 238 AA;

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ADA25215 standard; protein; 238 AA.

(first entry)

20-NOV-2003

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The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either profistion 65 or 122. The mutants of the invention acticularly F64L-S175G-E222G-CG PF (ADA25195) or F64L-S67T-S175G-GFP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous calls at temperatures above 30 degrees constitution, and excited at 490 nm. The mutants can also be detected in mamalian cells at lower levels of expression and with increased constitution relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle cusion, for vigualising translocation of intracellular proteins to a secretion markers as genetic reporters or protein and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FRCS), as real-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial celection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GFP sequence shown in the information given on page 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VTTLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEBLFTGVVPILVBLDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSKGEBLFTGVVPILVBLDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                               Green fluorescent protein; GFP; jellyfish; marker protein; reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IndelB
                                                                                                                                                                                            /note= "Gly replaces wild-type Glu"
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Pred. No. 5.5e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               (AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD.
(AMSH ) AMERSHAM BIOSCIENCES UK LTD.
                                                                                                                                    Location/Qualifiers
Misc-difference 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michael NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.24;
                                                                                                                                                                                                                                                                                                                      28-SEP-2001; 2001GB-00023288.
                                                                                                                                                                                                                                                                                                                                                              23-APR-2001; 2001GB-00009858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.2
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stubbs SLJ, Jones AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-095652/09.
                                                                                                               Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADA25193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238 AA;
                                                                                                                                                                                                                                        GB2374868-A.
                                                                                                                                                                                                                                                                              30-OCT-2002
                                                                                                Synthetic.
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detection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                            61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                     121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green fluorescent protein; GFP; jellyfish; marker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein mutant, F64L-S65T-S175G-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Gly replaces wild-type Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Leu replaces wild-type Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Thr replaces wild-type Ser"
                                                                                                                                                      99.2%; Score 1266; DB 6;
99.2%; Pred. No. 5.5e-124;
ive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA25196 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2001; 2001GB-00023288
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Matches 236; Conservative
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Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 64
                                                                                                                Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2003
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                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA25196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Aequorea victoria green fluorescent protein CC (GFP) mutants containing an amino acid subsitution at positions 64 and CG FP, mutants containing an amino acid subsitution at either proistion 65 or 222. The mutants of the invention are particularly F64L-S176G-E222G-CC GFP (ADA25195) or F64L-S65T-S176G-GFP (ADA25196). GFP mutants of the convention exhibit enhanced fluorescence relative to wild type GFP when CC Gaptions, and excited at 490 nm. The mutants can also be detected in companian cells at lower levels of expression and with increased CC ensaitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle CC fusion, for visualising translocation of intraocellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein contains and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers to be to see the combination with fluorescent activated cell sorting (FACS), as cell-time probes working at near physiological concentrations, for pacterial
HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                   Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                       Green fluorescent protein; GFP; jellyfish; marker protein; reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                Green fluorescent protein mutant, F64L-V163A-E222G-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Ala replaces wild-type Val"
Misc-difference 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Gly replaces wild-type Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Leu replaces wild-type Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michael NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                               ADA25223 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001GB-00023288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-2001; 2001GB-00009858.
                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; ADA25193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 163
                                                                                                                                                                                                                                                                                                                                                                                                                                       Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                            20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                       ADA25223;
                      121
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Claim 9; Fig 4; 52pp; English

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The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either proletion 65 or 222. The mutants of the invention are particularly F64L-S175G-E222G-GFP (ADA25195). GFP mutants of the invention are particularly F64L-S175G-E222G-GFP (ADA25195). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous cells at temperatures above 30 degrees celsius, and excited at 490 nm. The mutants can also be detected in communitation cells at lower levels of expression and with increased are useful as non-toxic markers for selection of transfected cells, as ensitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as genetic reporters to a specific organelle in living and fixed cells, as markers in call or organelle for visualising translocation of intracellular proteins to a specific organelle integrity markers, as transfection markers as markers to be used in combination with fluorescent activated cell sorting (FACS), as the probes working at near physiological concentrations, for parterial general sequence reporters for bacterial detection. The present sequence reporters for bacterial
                  88888888888888888888888888
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99.1%; Score 1265; DB 6; Length 238; 99.2%; Pred. No. 7e-124; ive 1; Mismatches 1; Indels Best Local Similarity 99.2 Matches 236; Conservative Sequence 238 AA; 61 Query Match

Gaps

VTTLSYGVOCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 9 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238 ö 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT 121 181 181 d ઠે 윰 g ઠ g ठ ò

Green fluorescent protein; GPP; jellyfish; marker protein; reporter protein; mutant; mutein. Green fluorescent protein mutant, S175G-GFP. ADA25214 standard; protein; 238 AA 20-NOV-2003 (first entry) ADA25214; RESULT 10 

/note= "Gly replaces wild-type Ser" Location/Qualifiers Key Misc-difference 175 Synthetic. Aequorea victoria.

GB2374868-A

30-OCT-2002

28-SEP-2001; 2001GB-00023288.

23-APR-2001; 2001GB-00009858

The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either profistion 65 or 122. The mutants of the invention are particularly F64L-S175G-E222G-CC GFP (ADA25195) or F64L-S67T-S175G-F6FP (ADA25 Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein. Thomas N; (AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD. (AMSH ) AMERSHAM BIOSCIENCES UK LTD. Michael NP, Example 2; Page; 52pp; English. Jones AE, 2003-095652/09 N-PSDB; ADA25193 SLJ, Stubbs 

Gape í o Length 238; Indels 99.1%; Score 1264; DB 6; 99.2%; Pred. No. 8.9e-124; iive 0; Mismatches 2; Best Local Similarity 99.2 Matches 236; Conservative Query Match

Sequence 238 AA;

61 VITLSYGVOCFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 121 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 1 MSKGEBLFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL g ઠે 셤 ઠે 8

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238 ઠ

셤

ABR44424 standard; protein; 238 11-JUL-2003 ABR44424; ABR44424 2X2X5X5X5X

RESULT 11

F64L-Y66H-S175G-GFP #SEQ ID 3.

Green fluorescent protein; GFP; marker; label; reporter; bacterial detection; mutein.

Green fluorescent protein; GFP; jellyfish; marker protein; reporter protein; mutant; mutein.

Green fluorescent protein mutant, F64L-GFP.

20-NOV-2003 (first entry)

ADA25212;

/note= "Leu replaces wild-type Phe"

Location/Qualifiers

Misc-difference 64

3B2374868-A 30-OCT-2002

Synthetic. Aequorea victoria.

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The invention relates to a fluorescent protein derived from Green

C fluorescent Protein (GPP), or any functional GPP analog having an amino
acid sequence which is modified by amino acid substitution compared with
the sequence which is modified by amino acid substitution compared with
the sequence which is modified by amino acid substitution compared with
the invention is useful for measuring the expression of a protein of
interest in a cell, and is also useful for determining the cellular
and/or extracellular localisation of a protein of interest. GPF's of the
invention are useful as non-toxic markers for selection of transfected
cells containing an expression vector encoding at least the fluorescent
protein. GPF's may also be used as protein labels in living and fixed
cells, as markers in cell or organelle fusion, for visualising
translocation of proteins fused to them, as secretion markers, as genetic
reporters or protein tags in transgenic animals, as cell or organelle
integrity markers, as markers to be used in combination with fluorescent
activated cell sorting (RAGS) and as reporters for bacterial detection.
GPF's are also useful for performing transposon mutagenesis, where the
superior succession of proteins present at low concentrations and are
suitable labels for proteins present at low concentrations. The current
of the invention have improved fluorescence properties and are
suitable labels corrected fluorescent protein (GFP) mutant F64L-Y66H-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel blue-shifted variants of green fluorescent protein having improved fluorescence properties, useful for measuring expression of a protein of interest in a cell, as a secretion, cell or organelle marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                     Ruehlmann D, Michael NP;
                                                                                                                                                                                                                                     (AMSH ) AMERSHAM BIOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Fig 3; 45pp; English.
                                                                                                                                                  27-SEP-2002; 2002WO-GB004354
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Matches 236; Conservative
                                                                                                                                                                                                                                                                                                   Jones AE, Davies J,
                                                                                                                                                                                                                                                                                                                                         WPI; 2003-421211/39
                        Aequorea victoria
                                                                                                                                                                                                                                                         (STUB/) STUBBS S.
                                                                WO2003029286-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 AA;
                                                                                                          10-APR-2003
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Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.

Thomas N;

(AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD. (AMSH ) AMERSHAM BIOSCIENCES UK LTD.

28-SEP-2001; 2001GB-00023288; 23-APR-2001; 2001GB-00009858. Stubbs SLJ, Jones AE, Michael NP,

WPI; 2003-095652/09. N-PSDB; ADA25193.

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The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either proistion 65 or 222. The mutants of the invention are particularly F64L-S175G-E22G-GFP (ADA25195) or F64L-S65T-S175G-GFP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous cells at temperatures above 30 degrees Celsius, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organilation fundants of the invention and selection of transled cells, as markers in cell or organilating fundants of the invention of protein labels in living and fixed cells, as markers in cell or organilation fundants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific organelle, as secretion markers, as genetic reporters or protein tags for protein and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as real-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents an Aequorea victoria GFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GPP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Score 1262; DB 6;
99.2%; Pred. No. 1.4e-123;
iive 0; Mismatches 2;
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Best Local Similarity 99.2
Matches 236; Conservative
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ADA25212 standard; protein; 238 AA

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RESULT 12 ADA25212 ö

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Claim 1, Page, 18pp; English
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Aequorea victoria green fluorescent protein (GPP) mutants containing an amino acid subsitution at positions 64 and cortaining an amino acid subsitution at either protistion 65 or 222. The mutants of the invention are particularly F641-S175G-E22G-CGP (ADA25195) or F641-S675-S175G-E22G-CGP (ADA25195) or F641-S675-S175G-E22G-CGP (ADA25195) or F641-S675-S175G-E326G-CGP (ADA25195) or F641-S675-S175G-E32G-CGP (ADA25195) or F641-S175G-CGP (ADA25195) or F641-S175G-CGP (ADA25195) or F641-S175G-CGP (ADA25
                                                                      NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                    181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                       Green fluorescent protein; GPP; jellyfish; marker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Ala replaces wild-type Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Gly replaces wild-type Glu"
                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein mutant, V163A-E222G-GPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UK LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMSH ) AMERSHAM PHARMACIA BIOTECH (AMSH ) AMERSHAM BIOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                   reporter protein; mutant; mutein.
                                                                                                                                                                                                                                           ADA25220 standard; protein; 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2001; 2001GB-00023288
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                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-095652/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria.
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                                                                                                                                                                                                                                                                                                             20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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real-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents an Aquorea victoria GFP mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                                                                                                                                  VTTLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green fluorescent protein; GFP; jellyfish; chromophore development; bioluminescent labeling; agriculture; nitrogen fixation; cheese; food production; anaerobic fermentation, alcoholic fermentation; yogurt; pickle; beer; methanol; fuel production; glycerol; sewage treatment; soil; detoxifying microbial agent; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGBELFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aequorea victoria green fluorescent protein (GFP), mutant F64M.
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                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                        Score 1262; DB 6;
Pred. No. 1.4e-123;
0; Mismatches 3;
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                                                                                                                                                                                                                          98.9%;
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                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                    Similarity
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Misc-difference
                                                                                                                                                                             Sequence 238 AA;
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                                                                                                                                                                                                                                                                          235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                          Query Match
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The invention relates to a green fluorescent protein (GFP) variant (I) exhibiting, under oxygen concentration that is equal or lower than camospheric, rapid chromophore development as compared with a wild-type (GFP. (I) is useful in in vitro, in situ or in vivo bioluminescent labeling, in any labeling applications in which GFP is currently used, in Situations where wild-type GFP is not stable i.e., high ionic strength buffers and/or high temperature, in haplophytes, thermophyes and in corganelles with varying salt and membrane compositions, and in corganelles with varying salt and membrane compositions, and in corganelles with varying salt and membrane compositions, and in coff low oxygen status in cells and tissues, and as detectable substance in coff low oxygen status in cells and tissues, and as detectable substance in coff low oxygen status in cells and tissues, and as detectable substance in coff low oxygen status in cells and tissues, and such of ermentation is utilised, including manufacturing of cheese, yogurt, correcting nethanol for fuel production or glycerol. (I) is useful for monitoring coxygen level in microbial degradation of municipal sewage treatment, for cesting an enzyme having a degradation of municipal sewage treatment, for condition, for monitoring microbial processes in a coll, and for monitoring cordition, for monitoring microbial agents. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                     VITMSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                  NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                        NRIELKGIDFKEDGNILGHKILEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                      Gapa
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98.7%; Score 1260; DB 5; Length 238; 98.7%; Pred. No. 2.3e-123;
                               Indels
                            1; Mismatches
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Phosphorylation indicator; fluorescent protein; detection; phosphatase; kinase; green fluorescent protein; GFP; mutant; mutein. Aequorea victoria mutant green fluorescent protein (8175G). Z AAE34996 standard; protein; 238 (first entry) 28-MAY-2003 AAE34996; RESULT 15 

Aequorea victoria. Synthetic.

'note= "Wild-type Ser substituted with Gly" Location/Qualifiers Misc-difference 175

WO200295058-A2

28-NOV-2002

24-MAY-2002; 2002WO-US016955.

24-MAY-2001; 2001US-00865291.

(REGC ) UNIV CALIFORNIA

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The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting hisses or phosphatases in a biological sample. They are also useful in phosphatase inhibitor. The present sequence is Aquorea victoria mutant green fluorescent protein (GFP, S175G) used in the invention. Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild-type GFP shown as SEQ ID NO: 2 in column 53-54 of the
                                                                                                       Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in
                                                                                                                                                                                                                       Disclosure; Col; 38pp; English
                       Zhang J;
                       Ting AY,
                                                                 WPI; 2003-148474/14
                                                                                                                                                                             operative linkage.
                       Tsien RY,
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Sequence 238 AA;

ô 61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMYLLGFVTAAGITHGMDELYK 238 1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL Gaps ; 0 Length 238; Indels Query Match 98.7%; Score 1260; DB 6; Best Local Similarity 98.7%; Pred. No. 2.3e-123; Matches 235; Conservative 1; Mismatches 2; ઠે 원 δ 셤 ò g ò 셤

Search completed: September 16, 2005, 17:16:10 Job time : 119 secs

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RESULT 2
US-08-679-865-2
| Sequence 2, Application US/08679865
| Patent No. 512137
| GENERAL INFORMATION:
| APPLICANT: Taien, Roger Y. |
| APPLICANT: Cubitt, Andrew B. |
| TITLE OF INVENTION: Assays for Protein Kinases Using |
| TITLE OF SEQUENCES: 48 |
| CORRESPONDENCE ADDRESS:
61
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Sequence 18, Appl
Sequence 1, Appl
Sequence 2, Appli
Sequence 10, Appl
Sequence 159, Appl
Sequence 4, Appli
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                                                                                                                      September 16, 2005, 17:08:27; Search time 31 Seconds (without alignments) 573.112 Million cell updates/sec
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Sequence 2, Ag
Sequence 16, A
Sequence 18, A
Sequence 2, Ag
Sequence 1, Ag
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Sequence 2, Al
Sequence 1, Al
Sequence 2, Al
Sequence 2, Al
Sequence 2, Al
                                                                                                                                                                                                                             1 MSKGEELFTGVVPILVELDG.......VLLGFVTAAGITHGMDBLYK 238
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Sequence 2,
Sequence 2,
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Sequence 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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PCT-US95-14692-2
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                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      Bw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                        protein search, using
                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                         US-10-757-624-3
1276
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Match Length
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Sequence 2, Appli
Sequence 2, Appli
Sequence 94, Appli
Sequence 96, Appl
Sequence 98, Appl
Sequence 100, App
Sequence 100, App
Sequence 100, App
Sequence 101, App
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Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
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; Sequence 2, Application US/08753143A
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Heim, Roger Y.
; TILE OF INVENTION: WODIFIED GREEN FLUORESCENT PROTEINS
; TILE REFERENCE: 07257/032003
; CURRENT APPLICANT: Heim, NODIFIED GREEN FLUORESCENT FROTEINS
; CURRENT PRILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENOTH: 238
; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-753-143-2
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Pred. No. 8.4e-129;
0; Mismatches 3;
         US-00-646-538-2
US-09-503-222-2
US-09-479-645A-94
US-09-479-645A-96
US-09-479-645A-106
US-09-479-645A-100
US-09-479-645A-100
US-09-479-645A-104
US-09-479-645A-104
US-09-479-645A-104
US-09-863-901-2
US-09-863-901-3
US-09-863-901-5
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Best Local Similarity 98.7
Matches 235; Conservative
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CURRENT APPLICATION DATA:
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APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Fluorescent Protein Substrates
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRTE: California
                                                                                                                        COUNTAIL USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,865
FILING DATE: 16-UUL-1996
CLASSIFICATION: 435
ATYONEY/AGENT INFORMATION:
NAME: Stocella, John S.
REGISTRATION NUMBER: 023072-069000
TELEPHONE: (415) 576-0300
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Patent No. 5925558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein US-08-679-865-2
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                                                                              STATE: Ca
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61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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Patent No. 5981200
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILNG DATE: J1.7AN-1997
FILNG DATE: J1.7AN-1997
ATYONEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REBERRICE/DOCKET NUMBER: 07257/041001/UC 96-160-2
TELECOMMUNICATION INFORMATION:
TELEBPONE: 619-678-5099
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07257/041001/UC 96-160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
98.6%; Score 1258; DB 2;
Best Local Similarity 98.7%; Pred. No. 8.4e-129;
Matches 235; Conservative 0; Mismatches 3;
                                                                                                                                                               023072-069200
                  US/08/680,876
APPLICATION NUMBER: US/08/680, ICASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: SLOTE11A, JOHN S. REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION: TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                          LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-680-876-2
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STATE: California
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61 VITLSYGVOCFSRYPDHMKRHDPPKSAMPEGYVQERTIFFKDDGNYKTRAEVKPEGDTLV 120
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98.7%; Pred. No. 8.4e-129;
tive 0; Mismatches 3;
                               Score 1258; DB 3;
Pred. No. 8.4e-129;
0; Mismatches 3;
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APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
                                 98.6%;
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US-09-094-359-2
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Matches 235; Conservative
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                                 Query Match
Best Local Simil
Matches 235; C
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US-09-172-063-2
US-08-753-144-2
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US-08-75-144-2

Sequence 2, Application US/08753144

Sequence 2, Application US/08753144

Patent No. 6066476

GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STREET: CA
COUNTRY: USA
                                                                                                                         Length 238
                                                                                                                                                              Indels
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MEDIUM TYPE: Diskette COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER I IM COMPACTIBLE COMPUTER: I IM COMPACTIBLE COMPUTER: I IM COMPACTIBLE COMPUTER: I IM COMPACTIBLE COMPUTER: PRELEXITION DATA:
APPLICATION NUMBER: US/08/753,144
PILING DATE: 20-NOV-1996
PILING DATE: 10-OCT-1996
APPLICATION NUMBER: 08/57,452
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: 08/37,915
FILING DATE: 13-NOV-1994
ATTORNEY,AGENT INPORMATION:
NAME: HAILE, LAB A.
REGISTRATION NUMBER: 38,347
REFERENCE/POCKET NUMBER: 38,347
REFERENCE/POCKET NUMBER: 38,347
TELECOMMUNICATION INPORMATION:
NAME: HAILE, LAB A.
REGISTRATION NUMBER: 38,347
TELERPHONE: 619/678-5099
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LINPORMATINE - 238 amino acids
                                                                                                                         Score 1258; DB 2;
Pred. No. 8.4e-129;
0; Mismatches 3;
                                                                                                                           Query Match
Best Local Similarity 98.7%;
Matches 235; Conservative
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PRAGMENT TYPE: internal
 ; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-553-2
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                                                                                                                                                                                                                                                                                                                                                         Length 238;
APPLICANT: Wachter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT PRILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
EARLIER PILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Taien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Absays for Protein Kinases Using
TITLE OF INVENTION: Pluorescent Protein Substrates
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CONDTRY: USA
ZIP: 94111-3834
COMPUTER: EIM PC compatible
OPERATING SYSTEM: PAC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/263,975
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            Query Match
98.6%; Score 1258; DB 3;
Best Local Similarity 98.7%; Pred. No. 8.4e-129;
Matches 235; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/679,865
FILING DATE: 16-ULL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307Z-069000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09263975
; Patent No. 6248550
                                                                                                                                                                                                                                                                                   i ORGANISM: Aequorea victoria
US-09-172-063-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES FILE REFERENCE: 07257/032001
CURRENT APPLICATION NUMBER: US/08/727,452A
CURRENT FILING DATE: 1996-03-20
EARLIER APPLICATION NUMBER: PCT/US95/14692
EARLIER APPLICATION NUMBER: PCT/US95/14692
EARLIER FILING DATE: 1996-11-13
EARLIER FILING DATE: 1994-11-10
NUMBER: PSECIENT NUMBER: US 07/337,915
NUMBER: PSECIENT FILING DATE: 1994-11-10
SOFTWARE: FASICEC for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
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Pred. No. 8.4e-129;
0; Mismatches 3;
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98.7%; Pred. No. 8.4e-129;
iive 0; Mismatches 3;
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Patent No. 6319669
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 238 amino acids TYPE: amino acid TOPLOGY: linear MOLEME.
                                                                                                                                                                                       98.6%;
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ORGANISM: Aequorea victoria
                                                                                                                                                                                                           Best Local Similarity 98.7 Matches 235; Conservative
                                                                                                                               ; MOLECULE TYPE: protein US-09-263-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger Y. APPLICANT: Heim, Roger
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Best Local Similarity 98.7
Matches 235; Conservative
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08-09-129-192C-74

Defent No. 6495664

Patent No. 6495664

GENERAL INFORMATION:
APPLICANT: Autrora Blosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
TITLE OF INVENTION: Pluorescent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AURO1270 (08366/031001)
CURRENT APPLICATION UNDER: US/09/129,192C
CURRENT APPLICATION UNDER: 1998-07-24

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.0

SEQ ID NO 74

LENGTH: 238
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                                                                                                                    61 VITLSYGVQCFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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Gaps
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Patent No. 6608189

GENERAL INPORMATION:
APPLICANT: Tai.en, Roger Y.
APPLICANT: Injopis, Juan
APPLICANT: Machter, Robeka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REPERENCE: 07277/071001
CURRENT APPLICATION NUMBER: US/09/602,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
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3; Indels
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  Mismatches
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  235; Conservative
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US-09-602-641-2
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Best Local 8
    Matches
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APPLICANT: Aurora Blosciences Corporation
APPLICANT: Cubit, Andrew B.
TITLE OF INVENTION: Pluoressent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AUROL270 (08366/031001)
CURRENT APPLICATION NUMBER: US/09/129,192C
CURRENT FILING DATE: 1998-07-24
SUPPREME PROTEIN NOWER: 1908-07-24
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VTTLSYGVQCFSRYPDHMKRHDPPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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Factor No. 6414119

GENERAL INCRANTION:

APPLICANT: Flather, Hugh

TITLE OF INVENTION: Rapidly Greening, Low Oxygen Mutant of

TITLE OF INVENTION: Let Aequorea victoria Green Pluorescent Protein

FILE REPERBNCE: RucC 99-0011

CURRENT APPLICATION NUMBER: US/09/418,785

CURRENT PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: 60/104,563

PRIOR APPLICATION NUMBER: 60/104,563

PRIOR APPLICATION NUMBER: 60/104,563

PRIOR PILING DATE: 1999-10-16

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: Prasher, D.C. et al.
AUTHORS: Primary Structure of the Aequorea victorea green-f
JOURNAL: Gene
VOLUME: 111
PAGES: 229-233
DATE: 1992-01-01
DATABASE ACCESSION NUMBER: Genbank M62653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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98.7%; Pred. No. 8.4e-129;
iive 0; Mismatches 3;
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GENERAL INFORMATION:
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Matches 235; Conservative
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'Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 238
TYPE: PRT
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US-09-129-192C-2
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                                RESULT 10
US-09-418-785-1
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Fatent No. 662749
Fatent No. 662749
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FUNORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/067101
CURRENT APPLICATION NUMBER: US/09/704,463
FILE REPERENCE: 07257/067101
CURRENT APPLICATION NUMBER: 08/094,359
PRIOR APPLICATION NUMBER: 09/094,359
PRIOR PRILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 238
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Pred. No. 8.4e-129;
0; Mismatches 3;
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98.7%; Pred. No. 8.4e-129;
iive 0; Mismatches 3;
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1996-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 238
TYPE: PRI
                                                                                                                                                                                Query Match
Best Local Similarity 98.7%;
Matches 235; Conservative
                                                                                                                                ; ORGANISM: Aequorea victoria
US-09-602-641-2
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US-09-704-463-2
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Best Local Similarity 98.7
Matches 235; Conservative
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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98.6%; Score 1258; DB 4;
Best Local Similarity 98.7%; Pred. No. 8.4e-129;
Matches 235; Conservative 0; Mismatches 3;
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Job time : 33 secs
                               RESULT 15
10S-10-024-686A-2
Sequence 2, Application US/10024686A
Patent No. 6800733
                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Aequorea victoria
US-10-024-686A-2
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Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                US-10-757-624-3
1276
1 MSKGEELFTGVVPILVELDG......VLLGFVTAAGITHGMDELYK 238
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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6 US-10-757-624-3
10 US-09-967-301-4
6 US-10-757-624-4
US-09-967-301-2
1 US-09-967-301-2
1 US-10-057-505-2
1 US-10-057-505-2
1 US-10-293-580-2
US-10-293-580-7
US-10-457-982-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 1812044 segs, 404927589 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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-178-	US-10-757-624-2	e	US-10-845-936A-34	US-09-899-954B-2	US-09-920-922-4	-09-852-0	US-09-900-345A-125		308-	0	10-121-258-	US-10-221-461-6	2	10-305-765-1	10-305-765-1	9	10-305	10-132-067-	-570-	10-370-	10-423		٩	10-753-405-	-113-	-10-845-484-	-986-	US-10-857-622-2	-931-304-10	US-11-041-806-125	1	8-10-676-42	US-09-899-954B-8	
16	16	17	16	6	σ	σ	10	10	10	10	14	14	14	14	14	14	14	15	15	15	15	15	16	16	16	16	16	17	18	20	15	16	σ	
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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1 MSKGBELFTGVVPILVBLDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1276; DB 10; Length 238; 100.0%; Pred. No. 1.3e-117; ative 0; Mismatches 0; Indels 0;
Sequence 3, Application US/09967301
Sequence 3, Application US/09967301
Publication No. US20030175859A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stubbs, Simon L.
APPLICANT: Jones, Anne B.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FILE REFRENCE: PAOLIL
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/967,301
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: GB 0109858.1
PRIOR APPLICATION NUMBER: GB 0109858.1
SOFTWARE: PATENTIN ONCS: 19
SOFTWARE: PATENTIN ONCS: 19
SOFTWARE: PATENTIN ONCS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Simi
Matches 238;
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: GB 0109858.1
PRIOR FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
LENGTH: 238
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.28
Matches 236; Conservative
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                      NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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100.0%; Score 1276; DB 16; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 238; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stubbs, Simon L. J.
APPLICANT: Stubbs, Simon L. J.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomes, Anne E.
APPLICANT: Thomes, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FLIE REFERENCE: PADI11
CURRENT APPLICATION NUMBER: US/10/757,624
PRIOR APPLICATION NUMBER: US 09/967,301
PRIOR FILING DATE: 2001-09-28
PRIOR PLING DATE: 2001-09-28
PRIOR PLING DATE: 2001-09-28
PRIOR PLING DATE: 2001-09-28
PRIOR PLING DATE: 2001-09-28
SOFTWARE: PATENT NUMBER: GB 0109858.1
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENT VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09967301
Publication No. US20030175859A1
GENERAL INFORMATION:
APPLICANT: Stubbs, Simon L.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FILE REFERENCE: PA0111
CURRENT APPLICATION NUMBER: US/09/967,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: synthetic protein US-10-757-624-3
                                                                                                                                                                                                                                                                                Sequence 3, Application US/10757624; Publication No. US20040138420A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                            121
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                                                                                                                                                                                                                                  61 VITLSYGVÇÇFSRYPDHMKRHDFFKSAMPEGYVÇERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                   Gaps
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OTHER INFORMATION: Description of Artificial Sequence: synthetic COTHER INFORMATION: protein US-09-967-301-4
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                                                                                           Length 238;
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                                                                                99.1%; Score 1265; DB 10;
99.2%; Pred. No. 1.6e-116;
iive 1; Mismatches 1;
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Pred. No. 1.6e-116;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4

US-10-757-624-4

Sequence 4, Application US/10757624

Publication No. US20040138420A1

GENERAL INFORMATION:
APPLICANT:
APPLICATION NUMBER: US/10/757,624

CURRENT FILING DATE:
APPLICATION NUMBER: US 09/967,301

PRIOR FILING DATE: 2001-09-28

PRIOR FILING DATE: 2001-09-28

PRIOR FILING DATE: 2001-04-23

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 4

LENGTH: 238
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Best Local Similarity 99.2%;
Matches 236; Conservative
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61 VITLSYGVQCFSRYPDHMKRHDPFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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APPLICANT: Testen, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
STREET: A011a
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windiws95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.6%; Score 1258; DB 10; Best Local Similarity 98.7%; Pred. No. 7.9e-116; Matches 235; Conservative 0; Mismatches 3;
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APPLICATION NUMBER: US/10/024,686
FILING DATE: 17-Dec-2001
PRIOR APPLICATION NUMBER: 09/057,995
                                                                                           Sequence 2, Application US/09967301
Sequence 2, Application US/09967301
PUDICARTON NO. US20030175853A1
GENERAL INFORMATION:
APPLICANT: Stubbs, Simon L.
APPLICANT: Jones, Anne E.
APPLICANT: Thomas, Nicholas
ITILE OF INVENTION: Fluorescent Proteins
FILE REPERRICE: PA0111
CURRENT FILING DATE: 2001-09-28
FRIOR APPLICATION NUMBER: US/09/967,301
CURRENT FILING DATE: 2001-09-28
FRIOR PRIOR PLILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/10024686; Publication No. US20020123113A1
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Aequorea victoria
US-09-967-301-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 238
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US-10-024-686-2
                                                                                         US-09-967-301-2
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                             NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                                                                181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                       1 MSKGRELPTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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98.6%; Score 1258; DB 9; Length 238;
Best Local Similarity 98.7%; Pred. No. 7.9e-116;
Matches 235; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Andrew B. Frotein Kinases Using FITLE OF INVENTION: Assays for Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: 08/679,865
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: SLOEALIA, JOHN 2, 944
REFERENCE/DOCKET NUMBER: 02307Z-069000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/99/884,681
FILING DATE: 19-JUN-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: AFPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                       Sequence 2, Application US/0984681
Patent No. US20020061546A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-884-681-2
                                                                                                                                                                                                                                RESULT 5
US-09-884-681-2
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
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Publication No. US20020164674A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: HELM, ROGER
APPLICANT: CUBITT, Andrew
TILLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGENT260-3
CURRENT APPLICATION NUMBER: US/10/057,505
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SEQ ID NO S: 31
LENGRIH: 238
LENGRIH: 238
LENGRIH: 238
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APPLICATION NUMBER: 08/727,452
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: 08/52/4692
FILING DATE: 11-OCT-1996
APPLICATION NUMBER: 08/337,915
FILING DATE: 11-NOV-1995
APPLICATION NUMBER: 08/337,915
FILING DATE: 10-NOV-1994
APTORNEY/AGENT INFORMATION:
NAME: 40.000
TELECOMMUNICATION NUMBER: 07257/032002
TELECOMMUNICATION NUMBER: 07257/032002
TELECOMMUNICATION: 619/678-5099
INFORMATION FOR EGY OID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
98.6%; Score 1258; DB 13;
Best Local Similarity 98.7%; Pred. No. 7.9e-116;
Matches 235; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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; ORGANISM: Aequorea victoria
US-10-057-505-2
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Best Local Similarity
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Score 1258; DB 13; Length 238; Pred. No. 7.9e-116;

98.68;

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APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Frotein Sensors of Post-Translational Modifications
FILE REFERENCE: AUROL270 (08366/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
PRIOR APPLICATION NUMBER: US/10/293,580
PRIOR PRIOR PILING DATE: 1998-07-24
SOFTWARE: PROPERTY OF THE SEQUENCE OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 74, Application US/10293580

Publication No. US20030170767A1

GENERAL INFORMATION

APPLICANT: Aurora Biosciences Corporation

TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications

FILE REFERENCE: AUROL270 (08366/031001)

CURRENT APPLICATION NUMBER: US/10/293,580

FRICK APPLICATION NUMBER: US/09/129,192
                                                                                                                                                                                                                        61 VITLSYGYQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                          61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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98.6%; Score 1258; DB 14; Length 238;
Best Local Similarity 98.7%; Pred. No. 7.9e-116;
Matches 235; Conservative 0; Mismatches 3; Indels 0
                        3; Indels
            Mismatches
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235; Conservative
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US-10-293-580-2
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; TYPE: PRT
; ORGANISM: Aequorea victoria
US-10-724-178-2
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ORGANISM: Aequorea victoria
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Best Local Similarity
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LENGTH: 238
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                                                                                                         ; TYPE: PRT
; ORGANISM: Aequorea green fluorescent protein phosphorylation mutant
US-10-293-580-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10457982

| Sequence 2, Application US/10457982
| Publication No. US20030212265A1
| GENERAL INFORMATION:
| APPLICANT: Teien, Roger Y.
| APPLICANT: Miyawaki, Ateushi
| APPLICANT: Liopis, Junes
| APPLICANT: Remington, S. Junes
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
| TITLE OF INVENTION: PLUORESCENT PROTEIN SENSORS
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
| TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
| FRICK PRILING DATE: 2003-06-09
| PRIOR APPLICATION NUMBER: 09/102,641
| PRIOR APPLICATION NUMBER: 09/112,063
| PRIOR APPLICATION NUMBER: 09/112,063
| PRIOR SEQ ID NOS: 38
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LEMCTH: 238
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PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SEQ ID NO 74
LENGTH: 238
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US-10-457-982-2
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Matches 235; Conservative
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61 VITLSYGVQCPSRYPDHMKRHDFPKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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FILE OF INVENTION: COMPLEMENTATION ASSAYS
FILE REPREBNCE: ODDYGO7
CURRENT APPLICATION NUMBER: US/10/724,178
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: US 60/461,133
PRIOR PLILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: Patentin version 3.0
SEQ ID NO 2.2
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                           1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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98.7%; Pred. No. 7.9e-116;
iive 0; Mismatches 3;
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APPLICANT: Stubbs, Simon L. J.
APPLICANT: Jones, Anne E.
APPLICANT: Michel, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FILE REFERENCE: PO111
CURRENT APPLICATION NUMBER: US/10/757,624
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 09/967,301
PRIOR PILING DATE: 2001-09-28
PRIOR PLING DATE: 2001-09-28
PRIOR FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                   Sequence 2, Application US/10724178; Publication No. US20040137528A1; GENERAL INFORMATION: APPLICANT: Odyssey Thera, Inc.
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Cuevas, William

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TYPE: PRT
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                                                                                                      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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                                               Length 238;
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                                                                              Indels
                                              DB 16;
                                          Score 1258; DB 16,
Pred. No. 7.9e-116,
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10505486
Publication No. US20050118639A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TILLE OF INVENTION: Determination of a ligand
FILE REFRENCE: P03-0006FCT
CURRENT APPLICATION NUMBER: US/10/505,486
CURRENT FILING DATE: 2004-08-20
PRIOR PILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: JP 2002-13949
PRIOR FILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-23
PRIOR FILING DATE: 2002-07-13
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
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US-10-845-956A-34
US-10-845-956A-34
Sequence 34, Application US/10845936A
Publication No. US20040234609A1
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Aequorea coerulescens
                                         Query Match
Best Local Similarity 98.7%;
Matches 235; Conservative
US-10-757-624-2
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US-10-505-486-3
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; OTHER INFORMATION: GFP-SELP47K: silk, elastin and green fluorescent protein peptides | US-10-845-936A-34
APPLICANT: Kunar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods FITE OF INVENTION: and Uges
FILE OF ORGERPA, DOCOGGRAPA, DOCOG
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98.7%; Pred. No. 6.7e-115;
ive 0; Mismatches 3;
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Job time : 114 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.74
Matches 235; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Bw model - protein search, using OM protein

Run on:

September 16, 2005, 17:06:47; Search time 24.5 Seconds (without alignments) 934.677 Million cell updates/sec

US-10-757-624-3 1276

1 MSKGEELFTGVVPILVELDG......VLLGFVTAAGITHGMDELYK 238 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

-	Description	green-fluorescent	hypothetical prote	leucyl-tRNA synthe	nitrogenase (BC 1.	coatomer complex a	leucine-tRNA ligas	iron-sulfur cofact	imidazoleglycerol-	protective surface	protective surface	DNA-directed DNA p	tRNA (uracil-5-)-m	synaptogamin o-p65	water-stress-induc		hypothetical prote	DNA topoisomerase	DNA-binding protei	calpain (EC 3.4.22	inter-alpha-trypsi	hypothetical prote	hypothetical prote	S-layer protein pr	oligoendopeptidase	dihydrolipoamide d	thioredoxin reduct		prot	cellulase (EC 3.2.
	ID	JQ1514	H72228	E82590	NICLMA	ERHUAH	H64102	E70390	E84941	JC4078	F64102	A36028	G81355	JH0414	S53488	AC0582	D71614	D83917	T06586	CIHUH2	JC5576	AD2052	C95338	JC4930	A99552	I40794	C81710	B24815	B90103	S29043
	8	н	~	N	-	-	~	~	7	~	7	-	7	~	7	~	~	~	N	-4	~	7	~	~	7	-	~	~	~	7
	Match Length	238	785	887	534	1224	861	370	353	797	808	2222	357	439	263	860	2573	655	632	700	889	281	531	874	613	578	312	422	502	941
* Query	Match	97.8	9.4	7.8	7.2	7.1	7.0	6.9	6.9	6.9	6.9	6.9	6.8	6.8	6.8	6.9	6.9	6.7	6.7	9.9	9.9	9.9	9.9	9.9		6.5		•	6.5	6.5
	Score	1248	107	99.5	92.5	90	89.5	88.5	88	87.5	87.5	87.5	87	87	86.5	86.5	86.5	85.5	85	84.5	84.5	84	84	84	83.5	83	82.5	82.5	82.5	82.5
Result	No.	7	7	٣	4	S	ø	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	. 29

IgA Pc receptor pr IgA Pc receptor pr	hypothetical prote alpha-amylase homo	lipoxygenase (EC 1 synergohymenotropi	hypothetical prote	ABC-type transport DNA-directed DNA p	hypothetical prote	procein widgit; / ( photosystem II chl	probable myosin he	NADH dehydrogenase	conserved hypothet	fructose-bisphosph
A60234 FCSOAG	T31049 T39539	T11852 S68225	C97354	E81317 JDVLHH	C64468	A88103 T06936	T41235	G84245	C64613	A11535
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1134	470	310	425	564 788	336	351 461	1516	389	393	653
6 6.5	6.4	4.4	6.4	4.4	6.3	. o	6.3	6.3	6.3	6.3
82.5 82.5	8 8	82 82	81.5	81.5	91	81 81	81	80.5	80.5	80.5
30	35	. e. c	36	37	39	4 4 0 1	42	43	44	45

## ALIGNMENTS

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		<ul> <li>hydromedusa</li> </ul>	
		[validated	
		protein	
_		n-fluorescent protein (validated)	A Property of the Party of the
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green-fluorescent protein (validated) - hydromedusa (Aequorea victoria)
Gispeciaes: Aequorea victoria
Gispeciaes: Osco-1999 #text change 09-Jul-2004
Gispeciaes: Osco-1999 #text change 09-Jul-2004
Gispeciaes: Jo1514; P00315; S48693; S51330; S51331
Gispeciaes: Dscherode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J.
A; Prenderson number: J092
A; Pritle: Primary structure of the Aequorea victoria green-fluorescent protein.
A; Reference number: J01514; MUID:92175527; PMID:1347277
A; Reference number: J01514
A; Residues: 1-107, S', 109-238 «PRA1>
A; Residues: 1-107, S', 109-238 «PRA1>
A; Residues: 1-107, S', 101-140, 'L', 142-218, 'V', 220-238 «PRA2>
A; Molecule type: mRNA
A; MRNA
A; Molecule type: MRNA
A; Molecule type:

A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 46-64;74-122;132-151;154-183;185-200 < FRA3>
R; Inouye, S.; Tauli, F.I.
FEBS Lett. 351, 211-214, 1994
A; Title: Bvidence for redox forms of the Aequorea green fluorescent protein.
A; Reference number: 848693; MUID:94364470; PMID:8082767
A; Accession: 848693
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'K', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'K', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'R', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'R', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 158-171, 'R', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 188-171, 'R', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 188-171, 'R', 173-238 < INO>
A; Residues: 1-24, 'Q', 26-156, 'P', 188-171, 'R', 173-238 < INO>
A; Reference number: 851330
A; Reference number: 851330
A; Reference number: 851330

A; Molecule type: mRNA A; Residues: 1-13,'V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R', A; Cross-references: EMBL:X83959; NID:g634008; PIDN:CAA58789.1; PID:g634009 A; Experimental source: clone gfp1

A;Accession: S5131 A;Molecule type: mRNA A;Residues: 1-24,'Q',26-29,'R',31-83,'L',85-153,'G',155-156,'P',158-171,'K',173-208,'Q' A;Cross-references: EMBL:X83960; NID:g634010; PIDN:CAA58790.1; PID:g634011

A;Experimental source: clone gfp2 R;Yang, F.; Mose, L.G.; Phillips Jr., G.N. submitted to the Brookhaven Protein Data Bank, August 1996 A;Reference number: A65622; PDB:1GFL

A; Contents: number: n

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A; Contents: annotation; X-ray crystallography, 1.9 angstroms C; Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C; Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C; Genetics:
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Nature 399, 323-329, 1999

Nature 399, 323-329, 1999

A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72200; MUID:99287316; PMID:10360571

A; Accession: H72228

A; Accession: Braliminary
A; Accession: Freliminary
A; Residues: 1-785 < ARN>
A; Residues: 1-785 < ARN>
A; Cross-references: UNIPROT:Q9X1V9; GB:AE001806; GB:AE000512; NID:g4982196; PIDN:AAD3669
C; Genetics:
A; Gene: TM1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Daceles: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H7228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                                                                                         61 VITESYGVQCFSRXPDHMKQHDFFKSAMPEGVVQSRTIFYKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 RIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGGVQLADH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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----EDP------IRGYIRKAQYSYGWD 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                  C,Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
F;65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F;66/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 107; DB 2; Length 785; 19.7%; Pred. No. 0.45; tive 33; Mismatches 70; Indels &
                                                                                                                                                                                                                                                                             Indels
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97.8%; Score 1248; DB 1;
Best Local Similarity 97.1%; Pred. No. 5.3e-99;
Matches 231; Conservative 4; Mismatches 3;
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Best Local Similarity
Matches 46; Conserva
                                                                                                       A; Introns: 69/3; 167/3
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leucyl-tRNA synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: E82590
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Astricle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Crostances: Insel, Acids, Ac
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NICLMA

NICLMA

NICLMA

NAILCTRATE names et dintrogenase alpha chain; nitrogenase component I alpha chain

C; Pateries: Clostridium pasteurianum

C; Date: 01-Sep-1981 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C; Accession: S07389; I40816; A00545

R; Wang, S. Z.; Chen, J.S.; Johnson, J.L.

Nucleic Acids Res. 15, 3395, 1987

A; Title: Nucleotide and deduced amino acid sequences of nifD encoding the alpha-subunit c

A; Reference number: S07389; MUID:87231095; PMID:3473447

A; Molecule type: DNA

A; Residence i = 534 cmAn>

A; Residence i = 534 cmAn>

A; Cross-references: UNIFROT: EMBL:Y00155; NID:940583; PIDN:CAA68349.1; PID:958099E
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7.8%; Score 99.5; DE
Best Local Similarity 23.2%; Pred. No. 2.3;
Matches 46; Conservative 28; Mismatches
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A'Gene: XF2176
C'Superfamily: leucine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-887 <SIM>
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A;Title: HEP-COP, a novel human gene whose product is highly homologous to the alpha-sub: A;Reference number: JC4668; MUID:96194806; PMID:8647451
                                                  A; Molecule type: mRNA
A; Residues: 1-1224 <CHO>
A; Cross-references: UNIPROT: P53621; GB:U24105; NID:g1638873; PIDN:AAB70879.1; PID:g10023
A; Experimental source: Hep3B hepatocellular carcinoma cell
R; Feurle, G.E.; Hamecher, G.; Kusiek, R.; Meyer, H.E.; Metzger, J.W.
Biol. Chem. 267, 22305-22309, 1992
A; Title: Identification of xenin, a xenopsin-related peptide, in the human gastric mucos
A; Reference number: A44317; MUID:93054515; PMID:1429581
                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-25 <FEU>
A;Experimental source: gastric mucosa
                                                                                                                                                                                   A; Accession: A44317
                                     A, Accession: JC4668
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284 CNFIGVDGIVETLRDMAKCPDD-PELTKR------TEEVIABEIAAIQDDLDYFKEKL 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | : | : | : | 335 QGKTACLYVGGSRSHTYMMLKSFGVDSLVAGFEPAHRDDYEGREVIPTIKIDADSKNIP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 EITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYGGMMKEMHDGTILLDDMNHHDMEVVLB 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 NVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TLKFIC--TTGKLPVPW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 92.5; DB 1; Length 534; 19.9%; Pred. No. 4.7; tive 39; Mismatches 97; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 BVK-----PEGDTLVNRIELKGIDFKEDGNILGHKLEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 ELDGDVNGHKFSVSGEGEGDATYGKL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 19.94
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 K 209
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A,Note: sequence extracted from NLSUS backbone (NCBIP:117018)
A,Note: sequence extracted from NLSUS as determined by immunoassay, rise after meals and it b,Note: plasma levels of xenin 25, as determined by immunoassay, rise after meals and it c;Genetics:
C;Genetics:
A,Gene: GDB:COPA, HEP-COP
A,CASS-references: GDB:4642787; OMIN:601924
A,Map position: 1q23-1q25
C;Superfamily: yeast componer complex alpha chain; WD repeat homology
C;Superfamily: yeast commons; plasma; stomach
F;1-25/Product: xenin 25 #status experimental <XNP>
F;5-38/Domain: WD repeat homology <WD2>
F;47-80/Domain: WD repeat homology <WD2>
F;47-125/Domain: WD repeat homology <WD3>
F;47-125/Domain: WD repeat homology <WD3>
F;47-125/Domain: WD repeat homology <WD3>
F;31-164/Domain: WD repeat homology <WD3>
F;21-1-25/Domain: WD repeat homology <WD5>
F;21-27/Domain: WD repeat homology <WD5>
F;21-27/Domain: WD repeat homology <WD5>
F;21-27/Domain: WD repeat homology <WD5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
NyAlternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Date: 18-Aug-1995 #text.
C;Date: 18-Aug-1995 #text.
C;Date: 18-Aug-1995 #text.
C;Date: 18-Aug-1995
C;Date: 18-Aug-1
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A;Cross-references: UNIPROT:P43827; GB:U32774; GB:L42023; NID:g1573942; PIDN:AAC22581.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 KGYPEVALHFVKDE---KTRFSLALECGNIEIALEAAKALDDKNCWEKLGEVALLQGNHQ 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 NVYIMADKQKNGIKVNF-----KIRHNIEDGGVQ--LADHYQQNTPIGDGPVLLPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 EGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIE-LKGIDFKEDGNILGHKLEYNYNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
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C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1224;
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---VSERVRILKNCGQKS----LAYLTAA--THGLDE 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 90; DB 25.9%; Pred. No. 23; ative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.2.
Best Local Similarity
Local 41; Conservative
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xenopsin-related peptide precursor

costomer complex alpha chain homolog - human N;Alternate names: HEP-COP; xenopain homolog; xenopain-related peptide N;Contains: xenin 25; xenopain-related peptide C;Species: Homo sapiens (man) C;Date: 10-May-1996 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004 C;Accession: JC4668; A44317 C;Accession: JC4668, A44317 Gene 169, 223-227, 1996

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A; Molecule type: DNA
A; Residues: 1-222 <SEW>
A; Residues: 1-222 <SEW>
A; Cross-references: EMBL: 271538; NID: 91302316; PIDN: CAA96169.1; PID: 91302317; GSPDB: GN00:
A; Experimental source: strain $288C
R; Sen-Gupta, M; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
R; Sen-Gupta, M; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
A; Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa-
A; Reference number: $65111; MUID: 96310631; PMID: 8740425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tRNA (uracil-5-)-methyltransferase (EC 2.1.1.35) Cj0831c [imported] - Campylobacter jeju
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: Gal355
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT: Q9PP92; GB:AL139076; GB:AL111168; NID:g6968128; PIDN: CAB7309; Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-221 <SEF>
A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A;Note: the nucleotide seguence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY 73
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R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996
A;Reference number: 863235
A;Accession: 863235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:POL2; DUN2; MIPS:YNL262w
A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map Position: 14L
C;Superfamily: DNA-directed DNA polymerase II
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 2222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: S65121
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 87; DB 2; Length 357;
24.8%; Pred. No. 8.2;
tive 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: trma; Cj0831c
A;Gene: trma; Cj0831c
C;Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
6.9%; Score 87.5; D
Best Local Similarity 28.2%; Pred. No. 81;
Matches 37; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 LPVPWP-TLVTTLSYGVQCFSRYPDHM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guery Match
Best Local Similarity 24.8%
Matches 30; Conservative
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A;Molecule type: DNA
A;Residues: 1-357 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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A36028
DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cerevisions DNA-directed DNA polymerase II chain A; protein N0825; protein YNL262 C; Species: Saccharomyces cerevision 10-Sep-1999 #text_change 09-Jul-2004 C; Accession: A36028; B36028; S60319; S63235; S65121
R; Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Cell 62, 1143-1151, 1990
A; Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A; Reference number: A36028; MUD: 90381771; PMID: 2163349
A; Reference number: A36028; MUD: 90381771; PMID: 2163349
A; Residues: 1-222 < MOR>
A; Residues: 12-222 < MOR>
A; Residues: 12-222 < MOR>
A; Residues: 12-216, YX, 1218-1221 < MO2>
A; Molecule type: protein
A; Residues: 1214-1216, YX, 1218-1221 < MO2>
A; Molecule type: protein
A; Residues: 1214-1216, YX, 1218-1221 < MO2>
A; Molecule type: protein
A; Residues: 1214-1216, YX, 1218-1221 < MO2>
A; Molecule type: protein
A; Residues: 12-224 < MOS
A; Residues: 12-224 < MOS
A; Residues: 12-225 < MOS
A; Molecule type: DNA
A; Reference number: S60909
A; Reference number: S60909
A; Rocession: S60919
A; Rocession: S60919
A; Residues: 1-221 < SBNA
A; Residues: 1-201 < SBNA
A; Residues: 1-201 < SBNA
A; Residues: 1-201 < SBNA
A; Residues: 
                                                                                                                                                                                                                                                                               protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Accession: F64102
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kalley, J.M.; Weidman, J.D., J. Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Till: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64102
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Reafdues: 1-808 < TIGR.
A; Cross-references: GB:L42023; TIGR:HI0917
C; Superfamily: protective surface antigen D-15
C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNYNS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNVYIMADKOK-NGIKVN----FKIRHN----IBDGGVQLADHYQQNTPIGDGPVLL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LG-GRVTI 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73; Indels
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                                                                                    594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
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Local Similarity 22.4%; Pred. No. 22;
Les 49; Conservative 34; Mismatches
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Best Local S
Matches 49
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completed: September 16, 2005, 17:21:02
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S53488
water-stress-inducible protein DS2 - Chaco potato
C; Species: Solanum chaccense (Chaco potato)
C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C; Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C; Accession: S33488
R; Silhavy, D.; Hutvagner, G.; Barta, B.; Banfalvi, Z.
Plant Mol. Biol. 27, S87-595, 1995
A; Title: Isolation and characterization of a water-stress-inducible cDNA clone from Sola A; Reference number: S53488; MUID:95201251; PMID:7894021
A; Accession: S53488
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mossiques: 1-263 <SIL>
A; Cross-references: UNIPROT:Q41300; GB:U12439; NID:9607904; PIDN:AAA86052.1; PID:9607905
                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-439 <WEN>
A;Cross-references: UNIPROT:P24506; GB:M64276; NID:g213110; PIDN:AAA49228.1; PID:g213111
A;Experimental source: electric organ
                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Readdues: 'MIV', 26-34; XX', 194-199,'X', 201-206;'X', 322-332,'D', 334-337 <WENI>
C,Superfamily: synaptotagmin; protein kinase C C2 region homology
C,Keywords: glycoprotein; membrane protein; synaptic vesicle
E,75-101/Domain: hydrophobic <HYD>
            ---FGVEFLTTKQE--LSITLLYHKNIE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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DAETGLTEGEDKERERAKEREKGKIQFSLDYDFQANQLTVGIIQAABLPALDMGGTSDPY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NVYIMADKOKN-GIKVN------FKIRHNIEDGGVQLA-----DHYQQNTP 187
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                                                                                                                                                                                                              15-Jan-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LVELDGDVNGHKFSVSGEGEDATYGKLTLKFICTTGKLPV-PWPTLVTTLSYGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%; Score 87; DB 2; Length 439; Best Local Similarity 20.1%; Pred. No. 11; Matches 58; Conservative 44; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGDGPVLLPD-----NHYLSTQSALSKDPNEKRDHMVLLGFVTAAG
                                                                                                                                                --DILVNRIBLKGIDFKEDGNI--LGHKLEYNYNSH-----
     74 LDFADEKICAFMPRLLEYLRQDNKLKEKL-
                                       D 173
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Gibbories: Salmonella enterica subsp. enterica subsp. enterica serovar Typhi (st. C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Authors: Parry C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Accession: ACOSS2
A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EDGNILGHKLEY---NYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEGDDNKYGEKTSYGDSGYGEKPSYGGDDNKYGEKTSYGNEEGGYGGGVGETTNYEENE 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIR 168
                                                                                                                                                                         GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKRHDFFKSAMPB
                                                                                                                                                                                                                                                                                                                                       GYVQERTIFFKDDGNYKTRAE------VKFEGDTLVNRIEL--KGIDFK-----
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                             Length 263;
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1 Similarity 23.7%; Pred. No. 29;
42; Conservative 20; Mismatches
                     6.8%; Score 86.5;
19.8%; Pred. No. 6.1
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                                                                                                                                                                                                                                                          GESEKTSTYGEKT------
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C,Superfamily: leucine-tRNA ligase
Query Match
Best Local Similarity 19.8*
Matches 50; Conservative
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Best Local Similarity
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GFP AEQVI
ID GFP AEQVI
AC P42212; Q17104; Q27903;
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                                                                                   6; Search time 115 Seconds (without alignments)
1059.781 Million cell updates/sec
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                                                                                                                                      US-10-757-624-3
1276
1 MSKGEELPTGVVPILVELDG......VLLGFVTAAGITHGMDELYK 238
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Q8
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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             1612378 segs, 512079187 residues
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                                                                                       September 16, 2005, 16:55:06
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Maximum Match 100%
Listing first 45 summaries
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GFP_AEQVI
Q8GHE4
Q8GHE3
Q93125
Q17105
Q17106
Q6YGZO
Q8WP95
                                                              - protein search, using sw model
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QBWTC9
QBWTC7
QBWTC7
QBWTC7
QGRYS7
QGRYS5
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Q95UA7
Q7ZOW5
Q963F5
Q6RXS4
Q7ZOW9
Q66PW1
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Q816J8
Q8MU48
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Perfect score:
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Maximum DB
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No.
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VITLSYGVQCFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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067z0w4
065z0w4
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SEQUENCE FROM N.A.
STRAIN=DSM2289;
Koranyi P., Berenyi M., Burg K.;
Submitred (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF324408; AAN86140.1; -.
HSSP; P4212; 1GFL.
GO, GO:006091; P:energy pathways; IEA.
InterPro; IPRO10917; GFP_ike.
InterPro; IPRO10918; GFP_related.
InterPro; IPRO10986; Green_fl_protein.
Pfam; PF01153; GFP; 1.
RPINTS; PR01229; GFPUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26914 MW; F84840FIF9064018 CRC64;
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Last annotation update)
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98.7%; Pred. No. 2.7e-94;
iive 0; Mismatches 3;
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Best Local Similarity 98.7<sup>1</sup>
Matches 235; Conservative
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MEDLINE=97299832; PubMed=9154981; DOI=10.1023/A:1005740823703; Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.; Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage."; Plant Mol. Biol. 33:989-999(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION. MEDLINE-99455509; PubMed-9782051; DOI=10.1016/S0969-2126(98)00127-0; Machter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99238303; PubMed=10220315; DOI=10.1021/bi9902182;
Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
Bisliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
"Structural and spectral response of green fluorescent protein
variants to changes in pH.";
Biochemistry 38:5296-5301(1999).

-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the
blue chemiluminescence of the protein aequorin into green
fluorescent light by energy transfer. Fluoresces in vivo upon
receiving energy from the Ca(2+)-activated photoprotein aequorin.
Absorbs light maximally at 395 nm and exhibits a smaller
absorbance peak at 470 nm. The fluorescence emission spectrum
peaks at 509 nm with a shoulder at 540 nm.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-94185810; PubMed-8137953; DOI=10.1016/0014-5793(94)80472-9;
Inouye S., Tsuji F.I.;
"Aequorea green fluorescent protein. Expression of the gene and fluorescence characteristics of the recombinant protein.";
FEBS Lett. 341:277-280(1994).
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92175527; PubMed=1347277; DOI=10.1016/0378-1119(92)90691-H;
Arasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93192221; PubMed=8448132;
Cody C.W., Prasher D.C., Westler W.M., Prendergast F.G., Ward W.W.;
"Chemical structure of the hexapeptide chromophore of the Aequorea
                                                                                               Aequorea victoria (Jellyfish).
Bukaryota, Metazoa, Chidaria, Hydrozoa, Hydroida, Leptomedusae,
                                                                                                                                                                                                                                                                             "Primary structure of the Aequorea victoria green-fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96355665; Pubmed=8703075;
Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
Remington S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98294543; PubMed=9631087;
Yang F., Moss L.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Biotechnol. 14:1246-1251(1996).
                        (Rel. 32, Last sequence update) (Rel. 45, Last annotation update)
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      Created)
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                                                          Green fluorescent protein.
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                                                                                                                                                                                                                                                                                                                 Gene 111:229-233(1992).
                                                                                                                                  Aequoreidae; Aequorea.
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Cormier M.J.;
01-NOV-1995 ()
01-NOV-1995 ()
25-OCT-2004 ()
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                                                                                Name=GFP;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   1EMB; X-ray; @=1-238.
1EMC; X-ray; A/B/C/D=1-238.
1EME; X-ray; @=1-238.
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1BFP; X-ray; @=1-238.
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/B/C/D=1-238.
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1/B/C=1-238.
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A=1-228.
SUBUNIT: Monomer
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1EMK;
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1HCJ;
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1JC1;
1KPS;
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1MYW;
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PDB;
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PDB;
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Pseudomonadaceae; Azomonas.
NCBI_TaxID=116849;
                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.3%; Score 1254; DB 2; Length 238; 98.3%; Pred. No. 5.6e-94; ive. 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                             Koranyi P., Berenyi M., Burg K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AR324407; AAN86139.1; -.
BMBL; AR324407; BAN86139.1; -.
BKSP; P42212; 1BSC.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR01984; GFP_related.
InterPro; IPR01984; GFP_related.
InterPro; IPR01986; Green fl_protein.
Pfam; PF01353; GFP; 1.
PRNTMS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26886 MW; EASA6F2IFBFB6E05 CRC64;
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Koranyi P., Bernyi M., Burg K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A7324405, AAN86137.1; -.
HSSP; P42312, 1BFP.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR011584; GFP_related.
InterPro; IPR010596; Green_fl_protein.
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Matches 234; Conservative
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                                               PRELIMINARY;
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R InterPro; IPR009017; GFP_1ike.

R InterPro; IPR000786; Green_fl_protein.

R PF01123; GFP; 1.

R PR1NTS; PR01229; GFLUORESCENT.

R Probom; PP013756; Green fl_protein; 1.

CROSSLAK 65 67 5-imidazolinone (Ser-Gly).

T CROSSLAK 100 100 F -> Y.

VARIANT 108 108 F -> Y.

VARIANT 141 141 L -> S.

T CONFLICT 2 2 S -> G (in Ref. 3).

T CONFLICT 25 25 H -> Q (in Ref. 2).

T CONFLICT 157 157 Q -> P (in Ref. 2).

T CONFLICT 157 157 B -> K (in Ref. 2).
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Best Local Similarity 98.3
Matches 234; Conservative
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238 AA;
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Brown A.J.P.;
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                                                                                                                                                                                                                                             Gaps
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Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                                                                                                                                                              Length 238;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF324406; AAN86138.1; -..
HSSP; P42212; IGFL.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_itke.
InterPro; IPR0011584; GFP_related.
InterPro; IPR001384; GFP_related.
InterPro; IPR01329; GFPi.
PERNITS; PR01229; GFLUORESCENT.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26887 MW; E081616BD2AF6188 CRC64;
                                                                                                                                                                                                                                   Indels
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
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Last annotation update)
                                                                                                                                                              98.2%; Score 1253; DB 2;
98.3%; Pred. No. 6.8e-94;
tive 0; Mismatches 4
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                                                                                                                                                                                            Best Local Similarity 98.3
Matches 234; Conservative
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61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Yeast-enhanced green fluorescent protein (yEGFP) a reporter of gene expression in Candida albicans.";
Microbiology 143:303-311(1997).
BMEL; U73901, AAB18957.1; -
PDB; 2YPP; X-ray; A=1-238.
GO; GO:000001; Penergy pathways; IEA.
InterPro; IPR0101584; GFP_related.
InterPro; IPR0101584; GFP_related.
InterPro; IPR0101584; GFP_related.
Fram; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
SEQUENCE 238 AA; 26840 MW; A28622809A9DEAGO CRC64;
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MEDLINE=56305137; PubMed=8707053; DOI=10.1016/0378-1119(95)00685-0;
Cormack B.P., Valdivia R.H., Falkow S.;
"FAGS-optimized mutants of the green fluorescent protein (GFP).";
                                                                                                                                                                                                                                                          Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae, Aequorea.
NCBI_TaxID=6100;
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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                                                                                                                      01-077-2003 (TrEMBLrel. 02, Last sequence update) 01-077-2003 (TrEMBLrel. 25, Last annotation update) Recen fluorescent protein mutant 3.
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Last annotation update)
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Best Local Similarity 97.5%; Pred. No. 2.1e-93;
Matches 232; Conservative 2; Mismatches 4;
         238 AA
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                                                                                          Created)
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                                                                        01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
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Similarity
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SEQUENCE FROM N.A.
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01-MAR-2002 (
01-MAR-2002 (
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Best Local Simi
Matches 217;
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QBWTC6
ID QBWTC
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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95.0%; Score 1212; DB 2; Length 238;
Best Local Similarity 94.1%; Pred. No. 1.5e-90;
Matches 224; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.8%; Score 1197; DB 2; Length 238; Best Local Similarity 93.3%; Pred. No. 2.4e-89; Matches 222; Conservative 7; Mismatches 9; Indels
           SEQUENCE FROM N.A.
Watkins J.N., Campbell A.K.;
Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X83959; GALS8789.1; -.
PIR; JS0692; JQ1514.
HSSP; P42212; IGFL.
GO; GO:006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR019584; GFP-related.
InterPro; IPR019584; GFP-related.
InterPro; IPR019584; GFP-related.
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Watkins J.N., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X89360; CA558790.1; -.
PIR; JS0692; JQ1514.
HSSP, P42212; 1BFP.
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                                                                                                                                                                                                                                                                                                     238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR0109017; GFP like.
InterPro; IPR011584; GFP_related.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP, 1.
PRINTS; PR01229; GFLUORESCENT.
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61 VITLSYGVQCFSRYPDHMKRHDPFKSAMPEGYVQERTIPPKDDGNYKTRAEVKFEGDTLV 120
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                          121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                                                                                                                                                                            MEDLINE=27726112; PubMed=12693991; DOI=10.1042/BJ20021966; Gurekaya N.G., Fradkov A.F., Pounkova N.I., Staroverov D.B., Bulina M.B., Yanushevich Y.G., Labas Y.A., Lukyanov S., Lukyanov K.A.; A. colourless green fluorescent protein homologue from the nonfluorescent hydromedusa Aeguorea coerulescens and its fluorescent
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Green fluorescent protein.
Aequore coerulescens (belt jellyfish).
Bukaryota; Metazoa; Gildaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
[1]
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EMEL; AY151052; AAN41637.1; -
HSSP; PA2212; 1B9C.
CO; GO:006091; F:energy pathways; IEA.
InterPro; IPR019594; GFP_related.
InterPro; IPR010586; Green_fl_protein.
Ffam; PF01353; GFP_11.
FRINTS; PR01229; GFLURESCENT.
FPCDOM; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26896 MW; DE72EDBB7ED9F9FE CRC64;
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(TrEMBLrel. 20, Last sequence update)
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1larity 91.2%; Pred. No. 2.8e-88;
Conservative 9; Mismatches 12;
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61 VITESYGIQCPARYPEHMKANDPPKSAMPEGYIQBRIIFFQDDGKYKIRGEVKFEGDILV 120
                                   VTILSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                        121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AP45433; AAL33918.1; -.

HSSP; P42212; 1KYP.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
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Aequoreidae, Aequorea.
NCBI_TaxID=147615;
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Q8WTD0;
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                                                                                          Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.;

Lid S.J., Xia N.S.;

Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.

EMBL, AF435431, AAL33916.1; --
HSSP; P42212; IKXP.

GO; GO:000501; P:energy pathways; IEA.

GO; GO:00501; P:energy pathways; IEA.

PEAM; PP01329; GPFLUORESCENT.

SEQUENCE 238 AA; 27015 MW; GB8FD75E88926903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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83.6%; Pred. No. 7.4e-82;
ive 19; Mismatches 20;
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83.2%; Pred. No. 1.6e-81;
ive 19; Mismatches 21;
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
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Best Local Similarity 83.2%
Matches 198; Conservative
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                                       Green fluorescent protein
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AC 08WP9
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DT 01-MA
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BE Green
GN Name
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              SEQUENCE FROM N.A.
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435427; AAL33912.1;
HSSP; P42212; IKYP.
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen I.L.G.J., Xia N.S.,
Lus K.J., Xia N.S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435429; AAL33914.1; -.
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Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomeduaae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Best Local Similarity 82.8%; Pred. No. 4.8e-81;
Matches 197; Conservative 19; Mismatches 22; Indels
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                                                                                                                                              GO; GO:0006091; P:energy pathways; IEA.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green £1 protein; 1.
SEQUENCE 218 AA; 26997 MW; 5F80A192173CB84D CRC64;
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Pfam; PP01353; GPP; L1.
PERINTS; PR01229; GPUORESCENT.
SEQUENCE 238 AA; 27047 MW; SP80A18FA1E7C84D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBWTCB,
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08WTC8
AC Q8WTC8
DT 01-MA
DT 
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61 VITLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGITHGMDBLYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                            (1]
SEQUENCE FROM N.A.
Luo W.K., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Luo W.K., Xia N.S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF415428; AAL33913.1;
HSSP; P42212; IKYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                             Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae, Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0006091; P:energy pathways; IBA.
Pfam; PP01353; GFP; 1.
PRINTS; PR01229; GFLUORRSCENT.
SEQUENCE 238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 1094; DB 2; 82.8%; Pred. No. 5.8e-81; artive 19; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: September 16, 2005, 17:20:07
ne : 117 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 82.8%
Matches 197; Conservative
                                                                                                                                                                                                    PRELIMINARY;
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September 16, 2005, 16:54:01; Search time 117 Seconds (without alignments) 786.743 Million cell updates/sec
                                                                                                                                                                                              US-10-757-624-4
1276
1 MSKGBELFTGVVPILVELDG........VLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                     2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                Title:
Perfect acore:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                            OM protein
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                       Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*	1: geneseqp1980s:*	enese	4: geneseqp2001s:*	 6: geneseqp2003as:*	7: geneseqp2003bs:*	8: geneseqp2004s:*
Database						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

5 ADA25212	38	99.2 238
AMM96322 AMM31879 ADA25195 ABG33268 AAM362199 AAM06304 AAW24037 AAW440479 AAW40470	22222222222222222222222222222222222222	

Aae16038 Aequorea	Abg32365 Aequorea	Abg75980 Jellyfish	Aae34999 Aequorea	~	_	Ada25217 Green flu	Ada25194 Aequorea		Adm78505 Wild-type		Adq59552 Aequorea	Ads17705 Green flu	Abb08630 GFP fusio	Abb08631 GPP fusio	Abb08632 GPP fusio	Abb08633 GFP fusio	Abb08634 GFP fusio	Ads17719 Green flu	Aaw48661 RG fusion
5 AAE16038	5 ABG32365	6 ABG75980	6 AAE34999	6 AAE34985	6 ABR44423	6 ADA25217	6 ADA25194	7 ADF70380	7 ADM78505	7 ADM78577	8 ADQ59552	8 ADS17705	5 ABB08630	5 ABB08631	5 ABB08632	5 ABB08633	5 ABB08634	8 ADS17719	2 AAW48661
238	238	238	238	238	238	238	238	238	238	238	238	239	432	441	450	468	477	491	554
98.9	98.9	6.86	6.86	6.86	6.86	6.86	6.86	6.86	98.9	6.86	98.9	98.9	6.86	6.86	6.86	6.86	98.9	6.86	98.9
1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262	1262
26	27	28	5	30	31	32	33	34		36	37	86	6	4 0	41	4.2	. 4 . 6	4	45

### ALIGNMENTS

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or 222. The mutants of the invention are particularly F641-S175G-E222G-GFP (ADA25196). GFP mutants of the convention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologue cells at temperatures above 30 degrees Celsius, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased sensitivity relative to wild type GFP. The GFP mutants of the invention created as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle fusion, for visualising translocation of intracellular protein to a specific organelle, as secretion markers, as genetic reporters or protein or organelle integrity markers, as transfected cells, as cell or organelle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as cell-time probes working at near physicological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents the specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria GFP mutant F64L-S65T-S175G-GFP
   8888888888888888888888888888888888
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Sequence 238 AA;

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61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                      61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                         NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGGVOLAD 180
                                                                                                                                                                                                                              1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                        Gaps
                                     í o
Query Match 100.0%; Score 1276; DB 6; Length 238; Best Local Similarity 100.0%; Pred. No. 2.1e-125; Matches 238; Conservative 0; Mismatches 0; Indels 0
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Green fluorescent protein mutant, F64L-S175G-GFP. ADA25218 standard; protein; 238 AA (first entry) 20-NOV-2003 ADA25218; RESULT 2 ADA25218 

Green fluorescent protein; GPP; jellyfish; marker protein; reporter protein; mutant; mutein. 'note= "Leu replaces wild-type Phe" Misc-difference 175 /note= "Gly replaces wild-type Ser" Location/Qualifiers Misc-difference 64 Synthetic. Aequorea victoria.

GB2374868-A.

30-OCT-2002.

28-SEP-2001; 2001GB-00023288

23-APR-2001; 2001GB-00009858

(AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD.

(AMSH ) AMERSHAM BIOSCIENCES UK LID

Michael NP, Thomas N; Stubbs SLJ, Jones AE,

WPI; 2003-095652/09. N-PSDB; ADA25193.

Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.

Example 2; Page; 52pp; English.

The invention relates to Aequorea victoria green fluorescent protein

(GFP) mutants containing an amino acid substitution at positions 64 and

(175, and additionally an amino acid substitution at either projetions 65

or 222. The mutants of the invention are particularly F64L-S175G-E222GGFP (ADA25195) or F64L-S65T-S175G-GFP (ADA25196). GFP mutants of the
invention exhibit enhanced fluorescence relative to wild type GFP when

expressed in non-homologous cells at temperatures above 30 degrees

consisted in non-homologous cells at temperatures above 30 degrees

consisted in non-homologous cells at temperatures on elected in

mammalian cells at lower levels of expression and with increased

consisted at a lower levels of expression and with increased

consisted at an anon-toxic markers for selection of transfected cells, as

protein labels in living and fixed cells, as markers in cell or organelle

consisted in the secretion markers, as genetic reporters or protein

consisted in combination with fluorescent activated cell sorting (RACS), as

consed in combination with fluorescent activated cell sorting (RACS), as

consed in combination with fluorescent activated cell sorting (RACS), as

consed in combination with fluorescent activated cell sorting (RACS), as

consed in combination with fluorescent activated cell sorting (RACS), as

creal-time probes working at near physiological concentrations, for

cells for the present sequence represents an Aequorea victoria GFP

contains the specification, but is derived from the wild-type GFP

contains the shown in Fig 2 and the information given on page 24.

Sequence 238 AA;

ö Gaps ö Length 238; Indels 0 Score 1272; DB 6; Pred. No. 5.4e-125; 1; Mismatches 99.7%;
Best Local Similarity 99.6%;
Matches 237; Conservative 1

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8

61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 ઠ 셤

121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 ઠે 유

HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 181 181 g ઠે

AAW76106 standard; protein; 238 AA AAW76106; AAW76106 

RESULT 3

(first entry) 18-NOV-1998

A. victoria green fluorescent protein mutant F64L/S65T.

Green fluorescent protein; GFP; mutant; jellyfish; excitation; chromophore. /note= "Gly replaces wild-type Ser"

Location/Qualifiers

```
Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                        Green fluorescent protein; GFP; jellyfish; marker protein; reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stubbs SLJ, Jones AE, Michael NP, Thomas N;
                                                                          Green fluorescent protein mutant, S175G-GPP
                                                                                                                                                                                                                                                                                                                                                                                                              (AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD. (AMSH ) AMERSHAM BIOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                28-SEP-2001; 2001GB-00023288.
                                                                                                                                                                                                                                                                                                                                                                               23-APR-2001; 2001GB-00009858
                                             20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-095652/09.
N-PSDB; ADA25193.
                                                                                                                                                                                                                               Misc-difference 175
                                                                                                                                                             Synthetic.
Aequorea victoria.
                                                                                                                                                                                                                                                                                GB2374868-A.
                                                                                                                                                                                                                                                                                                                 30-OCT-2002.
               ADA25214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a mutant green fluorescent protein (GFP) from Aequorea victoria in which a Phe residue at position 64 in the wild type protein is replaced by a Leu and a Ser at position 65 is replaced by a Try. These mutations occur in the chromophore region. GFP mutants are used in a method to discover GFP se mutated in the chromophore region that fluoresce more brightly than wild-type GFP upon excitation at 488 mm. These mutants can be used in a method for analyzing a cell containing the GFP. The GFP can also be fused to a protein and used to identify the intracellular localisation of a protein and used to identify the could be operatively connected to a coding portion encoding a mutant GFP could be operatively connected to a coding portion encoding a mutant GFP the from the cell then measures the effect of the stimulus on the regulatory element. NOTE: This sequence does not appear in the specification but has been constructed from the wild-type GFP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRIBLKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding mutant green fluorescent pigment proteins - with greater fluorescence intensity than wild-type proteins, useful for studying gene expression and protein localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTTLTYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFTGVVPILVELDGDVNGHKRSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
                                                                                               /note= "Wild-type Phe is replaced with Leu"
                                                                                                                    65
/label= 865T
/note= "Wild-type Ser is replaced by Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1270; DB 2;
Pred. No. 8.8e-125;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                     Valdivia RH, Falkow S;
                                                                                                                                                                                                                                                                                                                      (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5%;
                                                                                                                                                                                                                                                    97US-00791332
                                                                                                                                                                                                                                                                                     96US-0010960P
                                                                                 label= F64L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represented in AAW76106
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-505643/43.
   Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 238 AA;
                                                                 Misc-difference
                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                      31-JAN-1997;
                                                                                                                                                                                                                                                                                       01-FEB-1996;
                                                                                                                                                                                      US5804387-A.
                                                                                                                                                                                                                                                                                                                                                         Cormack BP,
                                                                                                                                                                                                                     08-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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The invention relates to Aequorea victoria green fluorescent protein (GFP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either protsition 65 or 122. The mutants of the invention are particularly F64L-S175G-E222G-CC GFP (ADA25195) or F64L-S67T-S175G-GFP (ADA25195) or GFG (ADA25195) or F64L-S67T-S175G-GFP (ADA25195) or GFG (ADA25195) or F64L-S67T-S175G-GFP (ADA25195) or GFG (ADA25195) or F64L-S67T-S175G-FP (ADA25195) or F64L-S67T-S175G-FP (ADA25195) or F64L-S67T-S175G-FP (ADA25195) or F64L-S67T-S175G-FP (ADA25195) or F64L-S67T-S175G-S175G-S175G-FP (ADA25195) or F64L-S67T-S175G-S175G-S175G-FP (ADA25195) or F64L-S67T-S175G-S175G-FP (ADA25195) or F64L-S67T-S175G-FP (ADA25195) or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1268; DB 6;
Pred. No. 1.4e-124;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.2
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ADA25214 standard; protein; 238 AA.

RESULT 4 ADA25214

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Gaps

. 0

Indels

; 0

Length 238;

Score 1267; DB 6; Pred. No. 1.8e-124; 2; Mismatches

99.3%; 99.2%;

9 9 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120

61

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 1 MSKGBBLFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 

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121 NRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKNNFKIRHNIEDGGVQLAD 180

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ureen iluorescent protein; GPP; jellyfish; gfpl0 gene; reporter;
humanise; expression; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aequorea victoria protein GFP10 mutant F65L+S65T
                                                                                                                                                                                                                                                                                                                                                                                            AAW22101 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1998 (first entry)
Query Match
Best Local Similarity 99.2<sup>3</sup>
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22101;
                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a fluorescent protein derived from Green

fluorescent Protein (GFP), or any functional GFP analog having an amino
acid sequence which is modified by amino acid substitution compared with
the sequence of wild type (wt) GFP. The polymucleotide encoding a GFP of
the invention is useful for measuring the expression of a protein of
the invention are useful for measuring the expression of a protein of
and/or extracellular localisation of a protein of interest. GFP's of the
cells containing an expression vector encoding at least the fluorescent
cells containing an expression vector encoding at least the fluorescent
colls, as markers in cell or organelle fusion, for visualising
cells, as markers in cell or organelle fusion, for visualising
cranslocation of proteins fused to them, as secretion markers, as genetic
creporters or protein tags in transgenic animals, as cell or organelle
creporters or protein tags in transgenic animals, as cell or organelle
creporters or protein for performing transposon mutagenesis, where the
creporters or so the invention have improved fluorescence properties
continued as a marker in transcriptional and translational fusions
continued as the continued of the contin
                      NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                         VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel blue-shifted variants of green fluorescent protein having improved fluorescence properties, useful for measuring expression of a protein of interest in a cell, as a secretion, cell or organelle marker.
                                                                                                                                       HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                     Green fluorescent protein; GPP; marker; label; reporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMSH ) AMERSHAM BIOSCIENCES UK LTD. (STUB/) STUBBS S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruehlmann D,
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                                                                                                                                                                                                                                                           ABR44424 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                           F64L-Y66H-S175G-GFP #SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 3; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2002; 2002WO-GB004354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2001; 2001GB-00023314.
                                                                                                                                                                                                                                                                                                                                                                                                                pacterial detection; mutein.
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davies J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-421211/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003029286-A1
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This sequence represents a mutant form of the green fluorescent protein GFP10 i.e. F641-865T. Green fluorescent proteins (GFP's) could be used as reporter molecules as they absorbs blue light and emits green light without requiring any coffactors, substrates, or additional gene products allowing GFP detection in living cells providing meaningful gene expression is achieved. By providing humanised GFP, adapted for expression in mammalian and human cells, problems associated with wildtype jellyfish GFP e.g. variable and low expression levels should be overcome. Note: The present sequence does not appear in the
                                                                                                                                                                                Humanised green fluorescent protein gene - optimised to provide high level expression in mammalian cells, used e.g. to label or identify cells, to locate proteins, etc.
Muzyczka N, Hauswirth WW;
                                                                                                                                                                                                                                                                                                                                                                               Claim 115; Page; 158pp; English.
                                                                                          WPI; 1997-385337/35.
Zolotukhin S,
                                                                                                                                                                                                                                                                                    cells,
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suitable labels for proteins present at low concentrations. The current sequence represents the green fluorescent protein (GFP) mutant F64L-Y66H-

Sequence 238 AA;

/label= 865T /note= "Wild-type Ser is replaced by Thr"

(UYFL ) UNIV FLORIDA RES FOUND INC.

97WO-US000755 96US-00588201

/label= F64L /note= "Wild-type Phe is replaced by Leu"

Location/Qualifiers

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WPI; 1999-132241/11.
N-PSDB; AAX08454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1998;
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                                                                                                                            VITLIYGVOCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                       61 VITLIYGVQCPSRYPDHAKQHDPPKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                   NRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                  121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                        9
                                                                                               MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                          HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                   Assays for protein kinase and modulators - using a fluorescent protein substrate which exhibits a different fluorescent property in the phosphorylated and un-phosphorylated state.
specification. It has been made by modifying the wild-type GPP10 amino acid sequence found in AAW31295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a green fluorescent protein variant from Aequorea victoria in which a wild-type Ser residue at position 65 is replaced with a Thr. This variant is used in a method to determine if
                                                                                      1 MSKGBELFTGVVPILVBLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                      Green fluorescent protein; protein kinase; phosphate donor;
phosphorylation; drug screening; receptor-ligand binding; signalling;
protein-protein interaction; kinase activation.
                                                                     Gaps
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                                                 Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "wild type Ser is replaced with Thr"
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                      A. victoria green fluorescent protein variant S65T.
                                               Score 1266; DB 2;
Pred. No. 2.3e-124;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                               AAW65078 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00679865.
96US-00680876.
96US-00680877.
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                                                99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= S65T
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                      Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cubitt AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-110616/10.
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Aequorea victoria.
Synthetic.
                                Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9802571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1997;
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                                                   Query Match
Best Local &
                                                                                                                                                                                                                                                          RESULT AAW65076
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contacting the sample with a phosphate donor (PD) and a fluorescent protein (PD) substrate for a PK, the protein substrate comprising a PF moiety and a phosphorylation site for a PK, where the protein substrate comprising a PF moiety and a phosphorylation site for a PK, where the protein substrate than in the un-phosphorylated state. The protein substrate is then the un-phosphorylated state. The protein substrate is then conspined and the amount of a fluorescent property that differs in the unphosphorylated state is resence of the protein substrate in amount that is consistent with the presence of the protein substrate in achod and products can be used in drug screening. They can be used for screening for compounds which affect cellular events, including receptoring and binding, protein interactions or kinase activation, which signal to the target kinase. NOTE: This sequence does not appear in the specification and has been constructed from the wild-type sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTTLTYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLBFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green fluorescent protein; gfp; jellyfish; Aequorea victoria; humanisation; reporter gene; substrate; cofactor; beta galactosidase; firefly luciferase; alkaline phosphatase; chloramphenicol acetyltransferase; CAT; beta glucuronidase; GUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEBLFTGVVPILVBLDGDVNGHKPSVSGEGEGDATYGKLTLKFICTTGKLPVPWFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1266; DB 2; Length 238;
Pred. No. 2.3e-124;
0; Mismatches 2; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised green fluorescent protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96328 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represented in AAW40479
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Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 238 AA;
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Humanised green fluorescent protein (9fp) genes can be used to identify transformed cells, to measure gene expression in vitro and in vivo, to label specific cells in multicellular organisms (e.g. to study cell ineage's), to label and locate fusion proteins, and to study cell intracellular trafficking. Commonly used reporter genes include betagalactosidase, firefly luciferase, alkaline phosphatase; chloramphenicol acetyltransferase (CAT), and beta glucuronidase (GUS). However, these have limitations in their use. Frequently, these reporter genes require the addition of a substrate and the size of certain proteins means that the expression of reporter fusion proteins can be difficult. The light stimulated GFP fluorescence is species independent and does not require any coffectors substrates or additional gene products from Aequorea victoria an as the GFP genes have been humanised, they are expressed a sufficient levels to be detectable in human cells, unlike previous GFP
      Humanised green fluorescent protein - used to measure gene expression and
                                                                                             Disclosure; Page 136-137; 152pp; English.
                                       identify transformed cells.
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Sequence 238 AA;

VITLIYGVQCESRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKIRAEVKFEGDILV 120 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180 9 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 HYQQNTPIGGGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLPVPWPTL Gaps , 0 Score 1266; DB 2; Length 238; Pred. No. 2.3e-124; 1; Mismatches 1; Indels ( 99.2%; Matches 236; Conservative Similarity 61 121 181 181 Query Match Local g 셤 ò ò 셤 à 용

AAE16042; 

AAE16042 standard; protein; 238 AA.

Location/Qualifiers Misc-difference

29-NOV-2001

Aequorea victoria GFP mutant protein (S65T). (first entry) 26-MAR-2002

Green fluorescent protein; cell lineage tracer; protein localisation; GRP; fusion tag; gene expression marker; fluorescent energy acceptor; immunoassay; hybridisation assay; fluorescent energy donor; biosensor; FRET; fluorescence resonance energy transfer; mutant; mutein.

Aequorea victoria. Synthetic.

/note= "Wild type Ser substituted with Thr"

WO200190147-A2

17-MAY-2001; 2001WO-US016149

19-MAY-2000; 2000US-00575847.

(UYOR-) UNIV OREGON STATE

Wachter R, Remington SJ;

New long wavelength engineered fluorescent proteins, useful as markers for gene expression, tracers of cell lineage or as fusion tags to monitor protein localization, or in detection assays, e.g. immunoassays or hybridization assays

Claim 2; Page; 181pp; English.

The patent discloses functional engineered fluorescent protein and its corresponding polymucleotide. The amino acid sequence of the engineered corresponding polymucleotide. The amino acid sequence of the engineered corresponding beneficial to Aequiversa green fluorescent proteins of the invention have varied fluorescent correspond to ion concentrations via a comparation in fluorescent characteristics. They are useful as markers for gene expression, tracers of cell lineage or as fusion tags to monitor protein localisation within living cells. The engineered fluorescent proteins are particularly useful for coupling engineered fluorescent proteins are particularly useful for coupling engineered fluorescent correction ansays, e.g. immunoassays or hybridisation assays. They are useful for tracking the movement of proteins in cells or in systems for detection assays, e.g. immunoassays or hybridisation assays. They are useful for tracking the movement of proteins in cells or in systems for detecting induction of transcription and for the simultaneous measurement of two or more processes within cells. Proteins of the invention are also useful as fluorescent energy donors or acceptors as well as biosensors for detecting anions. They crystal structure of the GFP is useful for designing mutants having altered fluorescent characteristics which are particularly useful for identify amino acids whose substitution alters the specificity and affinity of the binding conformation of the anion. The present sequence is Aequorea victoria conformation but is derived from Aequorea victoria wind type green specification but is derived from Aequorea victoria wild type green fluorescent protein shown in figure 3 of the specification (ABE16038)

Seguence 238 AA;

ö Gaps ö Length 238; 2; Indels 99.2%; Score 1266; DB 5; 99.2%; Pred. No. 2.3e-124; ive 0; Mismatches 2; Best Local Similarity 99.2 Matches 236; Conservative Query Match

1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL 1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT

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61 VITFIYGVQCFSRYPDH#KRHDFPKSAMPEGYVQERIIFPKDDGNYKTRAEVKFEGDTLV 120 121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 셤 ð g

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 ઠે g

ABG76008 standard; protein; 238 AA RESULT 10 ABG76008 BXXXE

30-APR-2003 (first entry)

ABG76008;

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The invention relates to a tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety (e.g. jellyfish care intoursecent protein, GFP) or a linker moiety that couples the donor and acceptor moieties. Also include are a recombinant nucleic acid coding for expression of the tandem fluorescent protein construct, an expression of the tandem fluorescent protein construct, an expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector, an expression determining whether a sample contains an enzyme or whether a compound alters the activity of an enzyme, determining the amount of activity of an enzyme, in a cell and testing for cleavage enzyme activity. The tandem construct is useful in enzymatic assays, using the principle of fluorescent resonance energy transfer (FRET) between the conting and acceptor moieties. The tandem fluorescent proteins are compound essential role in many disease processes e.g. Alzheimer's disease, hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent proteins were constructed comprising constructed comprising mutants of GFP with altered fluorescent sequence constructed comprising mutants of the inventor. Whete rhe present sequence of the inventor was repeated the present sequence of the inventor. The present sequence is not the inventor where we have the present sequence of the inventor where we have the present sequence of the inventor when the present sequence is not the present sequence in the present sequence in the present sequence is not the present sequence in the present sequence the present sequence in the present sequence a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shown in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing
                                                                                           fluorescent resonance energy transfer; tandem fluorescent protein; enzymatic assay; Alzheimer's disease; hypertension; inflammation; apoptosis; AlDS; acquired immunodeficiency syndrome; mutein.
                                                                           Jellyfish; enzyme; green fluorescent protein; GPP; FRET; mutant;
                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Ser substituted by Thr"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00594575.
97US-00792553.
99US-00396003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cubitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2002; 2002US-00057505.
                     Jellyfish GFP mutant S65T.
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                                                                                                                                                                                                                                                                                                           Misc-difference 65
                                                                                                                                                                                                       Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                                       US2002164674-A1
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31-JAN-1997;
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                                                                                                                                                                                                                                  Synthetic
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Query Match

Query Match

Query Match

Best Local Similarity 99.2%; Score 1266; DB 6; Length 238;

Best Local Similarity 99.2%; Pred. No. 2.3e-124;

Matches 236; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSKGEELFTGVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL 60

61 VITLIYGVQCFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60

8 8

The invention relates to Aequorea victoria green fluorescent protein (GPP) mutants containing an amino acid subsitution at either profetions 64 and 2175, and additionally an amino acid subsitution at either profetion 65 or 222. The mutants of the invention are particularly F64L-S175G-E222G-CC GPP (ADA25195) or F64L-S65T-S175G-GPP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when expressed in non-homologous cells at temperatures above 30 degrees collatus, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased sensitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as cuseful as non-toxic markers for selection of transfected cells, as greetific organelle, as secretion markers, as genetic reporters or protein complination with fluorescent activated cell sorting (FACS), as cused in combination with fluorescent activated cell sorting (FACS), as creation markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as creation markers, as markers for be cused in combination with fluorescent activated cell sorting (FACS), as creation markers, as markers for be creative probes working at near physiological concentrations, for real-time probes working at near physiological concentrations, for parterial NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180 121 NRIBLKGIDPKEDGNILGHKLBYNYNSHNYYIMADKQKNGIKVNPKIRHNIBDGSVQLAD 180 Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein. HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238 Green fluorescent protein; GFP; jellyfish; marker protein; reporter protein; mutant; mutein. /note= "Leu replaces wild-type Phe" Thomas N; Green fluorescent protein mutant, F64L-GFP. (AMSH ) AMERSHAM PHARMACIA BIOTECH UK LTD. (AMSH ) AMERSHAM BIOSCIENCES UK LTD. Michael NP, Location/Qualifiers ADA25212 standard; protein; 238 Example 2; Page; 52pp; English. 28-SEP-2001; 2001GB-00023288 23-APR-2001; 2001GB-00009858 (first entry) Stubbs SLJ, Jones AE, 2003-095652/09. Aequorea victoria. N-PSDB; ADA25193. Misc-difference 20-NOV-2003 30-OCT-2002. GB2374868-A. Synthetic. ADA25212; 121 181 RESULT 11 셤 ઠે a 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present sequence not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
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                                                                                                                                                                Length 238;
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                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                Score 1266; DB 6;
Pred. No. 2.3e-124;
1; Mismatches 1;
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                                                                                                                                                             99.2%;
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236; Conservative
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Aequorea victoria.
                                                                                                                  Sequence 238 AA;
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Example 2; Page; 52pp; English

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The invention relates to Aequorea victoria green fluorescent protein (GPP) mutants containing an amino acid subsitution at positions 64 and 175, and additionally an amino acid subsitution at either protein 65 or 222. The mutants of the invention are particularly F641-S175G-B222G-GFP (ADA25195) or F64L-S65T-S175G-GFP (ADA25196). GFP mutants of the invention are particularly F641-S175G-B222G-GFP (ADA25195) or F64L-S65T-S175G-GFP (ADA25196). GFP mutants of the invention expressed in non-homologous cells at temperatures above 30 degrees cells in non-homologous cells at temperatures above 30 degrees cells in non-homologous cells at temperatures above 30 degrees cells in non-homologous cells at temperatures above 30 degrees cells in non-homologous cells at temperatures and with increased cents censitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle (Lusion, for visualising translocation of intracellular proteins to protein and gene expression in transgenic animals, as cell or organelle integrity markers, as genetic reporters or protein combination with fluorescent activated cell sorting (FACS), as used in combination with fluorescent activated cell sorting (FACS), as cell-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
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99.2%; Pred. No. 2.3e-124;
ive 0; Mismatches 2;
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Aequorea victoria.
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Misc-difference

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transformed cells, to measure gene expression in vitro and in vivo, to transformed cells, to measure gene expression in vitro and in vivo, to label specific cells in multicellular organisms (e.g. to study cell ineage's), to label and locate fusion proteins, and to study cell intracellular trafficking. Commonly used reporter genes include betacalactorisate. Firefly luciferase, alkaline phosphatase; chloramphenicol acetyltransferase (GAT), and beta glucuronidase (GUS). However, these have limitations in their use. Frequently, these reporter genes require the expression of substrate and the size of certain proteins means that the expression of reporter fusion proteins can be difficult. The light stimulated GPP fluorescence is species independent and does not require any cofactors substrates or additional gene products from Aequorea victoria an as the GFP genes have been humanised, they are expressed at victoria an as the GFP genes have been humanised, they are expressed to sufficient levels to be detectable in human cells, unlike previous GFP
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                                                                                                                                                                                                                                                                        Humanised green fluorescent protein – used to measure gene expression and identify transformed cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%; Score 1266; DB 2; Length 247; 99.2%; Pred. No. 2.5e-124; ive 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .238
/label= S65T_GPP_variant
                                                                                                Hauswirth W;
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 142; 152pp; English.
                                                                                                    Zolotukhin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.2'
Matches 236; Conservative
                             (UYPL ) UNIV FLORIDA
                                                                                                                                                                       WPI; 1999-132241/11.
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Aeguorea victoria.
                                                                                                                                                                                                         N-PSDB; AAX08455
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                                                                                                    Muzyczka N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish)

green fluorescent protein (GFP) variants S65T and W7. W7 fluoresces at a shorter wavelength than GFP. The construct comprises a donor (e.g. S65T)

and an acceptor (e.g. W7) fluorescent protein moiety (donors and an acceptor present protein moiety (donors and a linker coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker moiety is a peptide coupling them. Preferably, the donor ing a protease cleavage site. In this can also a sample, the linker moiety contains many recognition sites for proteases, including trypsin, calpain and enterokinase. The donor and acceptor moieties exhibit fluorescent resonance energy transfer (FRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to is measured from the acceptor or donor moiety or maybe obtained using a activity of enzyme (in vivo and in vitro) and compounds altering enzyme ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and adding the linker moiety in the appropriate place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
          /label= S65C
/noce= wild type Ser substituted with Thr"
2399. -264
/label=_linker_moeity
                                                                                                                                                                                                                                                                                                                          /label= M153T
/note= "wild type Met substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                     /label= V161A
/note= "wild type Val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N212K
/note= "wild type Asn substituted with Lys"
                                                                                                                                                                                                                                                                          /label= N146L
/note= "wild type Asn substituted with Leu"
                                                                                                                                       258. 259
/label= trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                       'note= "wild type Tyr Bubstituted with Trp'
                                                                        250. .251
/label= trypsin_cleavage_site
253. .254
/label=_calpain_cleavage_site
                                                                                                                                                                        265. .501 . _ _ //label= W7_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cubitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US001457.
                                                                                                                                                                                                                           label= Y66W
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                                                                                                                                                                                                            Misc-difference 329
                                                                                                                                                                                                                                                                                                                                                              Misc-difference 426
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                                                                                                                                                                                                                                                            Misc-difference 409
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                                                                             Cleavage-site
                                                                                                            Cleavage-site
                                                                                                                                           Cleavage-site
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                                            Peptide
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Sequence 501 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                        NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVQLAD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                       MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                              Gaps
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Length 501;
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reporter protein; mutant; mutein.
                                                              2; Indels
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   DB 2;
   Score 1266; DB 2;
Pred. No. 7e-124;
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(AMSH ) AMERSHAM BIOSCIENCES UK LTD.
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   Query Match 99.2%;
Best Local Similarity 99.2%;
Matches 236; Conservative
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mammalian cells at lower levels of expression and with increased sensitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle tunion, for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein tags for protein and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as real-time probes working at near physiological concentrations, for performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents the specifically claimed Aequorea victoria GFP mutant F64L-S175G-E222G-GFP.
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and excited at 490 nm. The mutants can also be detected in
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                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 1265; DB 6; Length 238; 99.2%; Pred. No. 3e-124; ive 1; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 238 AA;
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Sequence 1, 1
Sequence 2, 1
Sequence 74,
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1276
1 MSKGEELFTGVVPILVELDG.......VLLEFVTAAGITHGMDELYK 238
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Sequence 2,
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(cgn2_6/ptodata/1/laa/5A_COMB.pep:*

(cgn2_6/ptodata/1/laa/5B_COMB.pep:*

(cgn2_6/ptodata/1/laa/6A_COMB.pep:*

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(cgn2_6/ptodata/1/laa/RECTUS_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-670-865-2
US-08-753-144-2
US-09-753-144-2
US-09-104-359-2
US-09-105-3-2
US-09-125-3-2
US-09-129-1926-2
US-09-129-1926-7
US-09-102-1926-2
US-09-102-1926-2
US-09-102-1926-2
US-09-102-1926-2
US-09-102-1936-2
US-09-102-1936-2
US-09-863-901-3
US-09-863-901-3
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                                                                                                                                                                                                513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
                                                                                                                  Title:
Perfect score:
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Maximum DB
                                              OM protein
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Appl
Appli
     Sequence 2, Ap
Sequence 1, Ap
Sequence 10, Ap
Sequence 159,
Sequence 4, Af
Sequence 2, Af
Sequence 2, Af
Sequence 2, Af
Sequence 2, Af
Sequence 5, Af
Sequence 5, Af
Sequence 5, Af
Sequence 5, Af
Sequence 94, Af
Sequence 94, Af
Sequence 94, Af
Sequence 96, Sequence 98, Sequence 98, Sequence 100,
                          US-00-479-645A-10
US-00-479-645A-159
US-09-472-065A-4
US-09-920-922-2
US-09-023-14692-2
US-09-023-946B-35
US-08-646-538-2
US-09-503-222-2
US-09-999-025A-2
US-09-479-645A-94
                                                                                                                  US-09-479-645A-98
US-09-479-645A-100
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**ALIGNMENTS** 

								Pro												
BSULT 1	18-08-893-327-16	Seguence 16, Application US/08893327	Patent No. 6020192	GENERAL INFORMATION:	APPLICANT: Zolotukhin, Sergei	APPLICANT: Hauswirth, William W.	APPLICANT: Muzyczka, Nicholas		TITLE OF INVENTION: Genes and Methods	NUMBER OF SEQUENCES: 20	CORRESPONDENCE ADDRESS:	ADDRESSEE: Arnold, White & Durkee	STREET: P. O. Box 4433	CITY: Houston	STATE: TX	COUNTRY: USA	ZIP: 77210-4433	COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk	COMPTEND TON DO COMPANY OF

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,327 FILING DATE:

CLASSIFICATION 1514
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:

NAME: Xitchell, Barbara S.

REGISTRATION NUMBER: 33,928
REGISCOMMUNICATION INFORMATION:

TELEPHONE: (312) 48-3000
TELEPAX: (713) 789-2679
INPORMATION FOR ERQ ID NO: 16: SEQUENCE CHARACTERISTICS:

LENGTH: 238 amino acide
TYPE: amino acide
TYPE: mino acide
TYPE: MOLECULE TYPE: protetin
US-08-083-327-16

Gaps ö Query Match 99.2%; Score 1266; DB 3; Length 238; Best Local Similarity 99.2%; Pred. No. 2.8e-130; Matches 236; Conservative 1; Mismatches 1; Indels

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60

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USA
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                                                                         NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKOKNGIKVNFKIRHNIEDGGVQLAD 180
                                                                                                                                                  VTTLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
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; Patent No. 6020192
; GENERAL INFORMATION:
    APPLICANT: Zolotukhin, Sergei
    APPLICANT: Hausewirth, William W.
    APPLICANT: Muzyczka, Nicholas
    TITLE OF INVENTION: Humanized Green Pluorescent Protein
    TITLE OF INVENTION: Genes and Methods
    NUMBER OF SEQUENCES: 20
    CORRESPONDENCE ADDRESS:
    ADDRESSEB: Arnold, White & Durkee
    STREET: P. O. Box 4433
    COTT: Houston
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99.2%; Pred. No. 3e-130;
iive 1; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION 514
PICASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 0FLA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (713) 789-2679
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 247 amino acids IYPE: amino acid
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Best Local Similarity 99.2
Matches 236; Conservative
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COUNTRY: USA
ZIP: 77210-4433
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                                61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                      190 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 247
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Sequence 2, Application US/08679865;
Fatent No. 5912137;
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
TITLE OF INVENTION: Riucrescent Protein Kinases Using TITLE OF INVENTION: Fluorescent Protein Substrates NUMBER OF SEQUENCES: 48;
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                US-08-753-143-2

Sequence 2, Application US/08753143A

GENERAL INFORMATION:

APPLICANT: Taien, Roger Y.

TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS

FILE REFERENCE: 07257/032003

CURRENT APPLICATION UNMER: US/08/753,143A

CURRENT FILING DATE: 1996-11-20
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,865
FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1262; DB 1;
Pred. No. 7.8e-130;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 238
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Best Local Similarity 98.7%;
Matches 235; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; ORGANISM: Aequorea victoria
US-08-753-143-2
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amino acid
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Patent No. 5925558
GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Substrates
TITLE OF INVENTION: Pluorescent Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,876
FILING DATE: 16-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307Z-069200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                 02307Z-069000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REPRENCE/DOCKET NUMBER: 0230:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
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TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 pmit
                                                                                                                                                                                                      : 238 amino acids amino acids
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Best Local Similarity 98.7
Matches 235; Conservative
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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61 VITLIYGVÇÇFSRYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                                    Query Match
98.9%; Score 1262; DB 2; Length 238;
Best Local Similarity 98.7%; Pred. No. 7.8e-130;
Matches 235; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08792553
; Sequence 2, Application US/08792553
; Patent No. 5981200:
; Patent No. 5981200:
; APPLICANT: Taien, Roger Y.
; APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IndelB
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEFORM: 619-678-5070
TELEFRAX: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

98.9%; Score 1262; DB 2;
Best Local Similarity 98.7%; Pred. No. 7.8e-130;
Matches 235; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-172-063-2
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                                           VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                   NRIELKGIDPKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                                                                                                                             HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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                                                                                                                                                                                                                                                                                             US-08-753-144-2

Sequence 2, Application US/08753144

Patent No. 606476

GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION:
CORRESPONDENCES:
ADDRESSEE: Fight & Richardson P.C.
ADDRESSEE: Fish & ADDRESSEE:
ADDRESSEE: Fish & Richardson P.C.
ADDRESSEE: Fish & ADDRESSEE:
ADDRESSEE: Fish & Richardson P.C.
ADDRESSEE: Fish & Richardson P.C.
ADDRESSEE: Fish & ADDRESSEE:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EMA COMPACTIBLE
OPERATING SYSTEM: Windiws95
OPERATING SYSTEM: Windiws95
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,144
FILING DATE: 20-NOV-1996
PRIOR APPLICATION NUMBER: 08/37,452
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: 08/37,452
FILING DATE: 113-NOV-1995
APPLICATION NUMBER: 08/33,915
FILING DATE: 10-NOV-1994
ATTOMER Haile Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/032002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-509
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TYPE: amino acid
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98.7%;
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Best Local Similarity 98.7
Matches 235; Conservative
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FRAGMENT TYPE: internal
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61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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Sequence 2, Application US/09172063
FACENT NO. 6150176
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Machter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENITON: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENITON: MESCRING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 0725/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
EARLIER FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAMY IN COMPANDATION:
JAPPLICANT: HIVAWAKI, Atsushi
JAPPLICANT: Hiyawaki, Atsushi
JAPPLICANT: Hiyawaki, Atsushi
JAPPLICANT: LIOPIS, Juan
JAPPLICANTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
JAPPLICANTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
JURENT APPLICANTION NUMBER: US/09/094,359
JUNERRY FILLING DATE: 1998-06-09
JUNERRY FILLING

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Patent No. 6140132
GENERAL INFORMATION:
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; ORGANISM: Aequorea victoria
US-09-094-359-2
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LENGTH: 238
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                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09263975

Patent No. 6248550
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Talen, Roger Y.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Pluorescent Protein Substrates
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,975
                                           Score 1262; DB 3;
Pred. No. 7.8e-130;
1; Mismatches 2;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/679,865
ATTORNEY/AGENT INFORMATION:
NAME: S.COCTELL-1996
ATTORNEY/AGENT INFORMATION:
NAME: S.COCTELL-1996
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                           Query Match 98.9%;
Best Local Similarity 98.7%;
Matches 235; Conservative
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amino acid
; ORGANISM: Aequorea victoria
US-09-172-063-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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61 VTTLTYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
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                                                                        VTTLTYGVQCFSRYPDHMKRHDFFKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                   APPLICANT: Telen, Roger Y.
APPLICANT: Helm, Roger Y.
APPLICANT: Telen, Roger Y.
TITLE OF INVENTION: FIUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES FILE REFERENCE: 07257/032001
CURRENT APPLICATION NUMBER: US/08/727,452A
CURRENT FILING DATE: 1996-03-20
EARLIER APPLICATION NUMBER: PCT/US95/14692
EARLIER PILING DATE: 1995-11-13
EARLIER APPLICATION NUMBER: US 07/337,915
EARLIER PILING DATE: 1994-11-10
SEALISE PILING DATE: 1994-11-10
SEQ ID NOS: 5
SOFTWARE: FABELSEQ for Windows Version 3.0
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US-09-418-785-1
Sequence 1, Application US/09418785
Patent No. 6414119
GENERAL INFORMATION:
TITLE OF INVENTION: Rapidly Greening, Low Oxygen Mutant of TITLE OF INVENTION: the Aequorea victoria Green Fluorescent Protein; FILE REFERENCE: RutC 99-0011
CURRENT APPLICATION NUMBER: US/09/418,785
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/104,563
PRIOR FILING DATE: 1998-10-16
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98.9%; Score 1262; DB 3; Length 238;
Best Local Similarity 98.7%; Pred. No. 7.8e-130;
Matches 235; Conservative 1; Mismatches 2; Indels
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Sequence 2, Application US/08727452A
Patent No. 6319669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aequorea victoria
US-08-727-452-2
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Best Local Similarity
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Sequence 74, Application US/09129192C

Sequence 74, Application US/09129192C

Sequence 74, Application US/09129192C

Sequence 74, Application US/09129192C

GENERAL INFORMATION:

APPLICANT: Cubitt, Andrew B.

TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications

FILE REFERENCE: AUROL270 (08366/031001)

FURENT APPLICATION VMBER: US/09/129,192C

CURRENT APPLICATION VMBER: 1998-07-24

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.0

SEQ ID NO 74

LENGTH: 238
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                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Aequorea green fluorescent protein phosphorylation mutant
US-09-129-192C-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Taien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Liopis, Juan
APPLICANT: Machter, Rebekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLOORSCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.9%; Score 1262; DB 4; Best Local Similarity 98.7%; Pred. No. 7.8e-130; Matches 235; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1262; DB 4;
Pred. No. 7.8e-130;
1; Mismatches 2;
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CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASLSEQ for Windows Version 4.0
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09602641 Patent No. 6608189
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Best Local Similarity 98.7%;
Matches 235; Conservative
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; ORGANISM: Aequorea victoria
US-09-602-641-2
                                                                                                                               RESULT 14
US-09-129-192C-74
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US-09-602-641-2
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Patent No. 649564
GENERAL INFORMATION:
APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Pluorescent Protein Sensors of Post-Translational Modifications
FILE REPERENCE: AUROL270 (08366/031001)
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.0
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                                                                                                 TYPE: PRT
OGGNISM: Aequorea victoria
PUBLICATION INFORMATION:
AUTHORS: Prasher, D.C. et al.
TITLE: Primary structure of the Aequorea victorea green-f
JOURNAL: Gene
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98.7%; Pred. No. 7.8e-130;
iive 1; Mismatches 2;
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DATABASE ENTRY DATE: 1993-04-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.79
Matches 235; Conservative
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Best Local Similarity 98.73
Matches 235; Conservative
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ORGANISM: Aequorea
                                                                                                                                                                                                                                                                                       PAGES: 229-233
DATE: 1992-01-01
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Search completed: September 16, 2005, 17:22:10 Job time : 31 secs THIS PAGE BLANK (USPTO)

us-10-757-624-4.rapb

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September 16, 2005, 17:20:18; Search time 113 Seconds (without alignments) 852.856 Million cell updates/sec
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10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1276
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	å Query Match Length DB	DB	ΩI	Description	
	1276	100.0		101	US-09-967-301-4	Sequence 4, Appli	
64	1276	100.0		16	US-10-757-624-4		
'n	1265	99.1		10	US-09-967-301-3		
4	1265	99.1		16	US-10-757-624-3	Sequence 3, Appli	
ហ	1262	98.9		σ	US-09-884-681-2	Sequence 2, Appli	
v	1262	98.9		10	US-09-967-301-2	Seguence 2, Appli	
7	1262	98.9		13	US-10-024-686-2	Sequence 2, Appli	
60	1262	98.9		13	US-10-057-505-2	Sequence 2, Appli	
6	1262	98.9	238	14	US-10-293-580-2	Sequence 2, Appli	
10	1262	98.9		14	US-10-293-580-74	Seguence 74, Appl	
11	1262	98.9		15	US-10-457-982-2	Sequence 2, Appli	

999	Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	, , , , , , , , , , , , , , , , , , ,	Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli	9,0,0	9,4,6	Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	1, 4	
10-668-168	US-10-757-624-2 US-10-505-486-3 US-09-863-901-1 US-10-207-380-1	2000	US-10-307-389-3 US-09-863-901-4 US-10-307-389-4	US-10-307-389-5 US-09-863-901-6 US-10-307-389-6	US-10-001-486B-2 US-10-259-864-4 US-10-845-936A-34	US-10-259-864-1 US-10-050-673-2 US-09-899-954B-2 US-10-422-628-2	US-10-668-168-6 US-09-920-922-4 US-09-852-000-1 US-09-900-345A-125	38-2 08-2 91-2 58-10 61-6 65-10
15	1225	1343	4045	404	14 16	14 13 9	51 6 6 5	2222444
238	238 438 535	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 6 8 4 5 0 4 6 8 8 4 6 8 4 6 8 4 6 8 4 6 8 4 6 8 4 6 8 4 6 8 4 6 8 6 8	477 906 906	1099	1147 1452 238 238	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	888888888888888888888888888888888888888
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#### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                    US-10-79-76-24-6

US-10-79-76-24-6

Publication No. US20040138420A1

GENERAL INFORMATION:
APPLICANT: Stubbs, Simon L. J.
APPLICANT: Jones, Anne E.
APPLICANT: Homes, Nicholas
FILE REFERENCE: PA0111
CURRENT APPLICATION NUMBER: US/10/757,624

CURRENT APPLICATION NUMBER: US/967,301

PRIOR FLING DATE: 2001-09-28

SOFTWARE FOR THE STATE STON-09-28

SOFTWARE PRIOR FLING DATE: 2001-09-28

SOFTWARE PRIOR PRIOR DATE: 2001-09-28

SOFTWARE PRIOR FLING DATE: 2001-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: synthetic protein
US-10-757-624-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 238; Conservative
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US-09-967-301-3
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US-10-757-624-4
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                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: protein
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                                                                                                                                                                                                                                                                                                  Score 1265; DB 10; Length
Pred. No. 7e-118;
1; Mismatches 1; Indels
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99.1%; Score 1265; DB 16;
Best Local Similarity 99.2%; Pred. No. 7e-118;
Matches 236; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stubbe, Simon L. J.
APPLICANT: Stubbe, Simon L. J.
APPLICANT: Jones, Anne E.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TILE REFERENCE: PAO111
CURRENT APPLICATION NUMBER: US/10/757,624
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 09/967,301
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SERIOTHM: 238
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: GB 0109858.1
PRIOR FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 3
LENGTH: 238
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; OTHER INFORMATION: synthetic protein
US-10-757-624-3
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.2%;
Matches 236; Conservative 1
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ORGANISM: Artificial Sequence
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APPLICATION NUMBER: 09/057,995
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Best Local Similarity 98.7%;
Matches 235; Conservative
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, ORGANISM: Aequorea victoria
US-09-967-301-2
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NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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                                                                      181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
MEDIUM TYPES: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSUT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,681
FILING DATE: 19-Jun-2001
CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION NUMBER: 08/679,865
                                                                                                                                                                                                 Sequence 2, Application US/09884681
Patent No. US20020061546A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using Fluorescent Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.9%; Score 1262; DB 9;
ilarity 98.7%; Pred. No. 1.4e-117;
Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: SCIOCALIA. JOHN S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 023072-069000
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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235; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-884-681-2
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US-09-884-681-2
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Best Local S:
Matches 235,
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VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQBRIIFFKDDGNYKTRAEVKFEGDTLV 120
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APPLICANT: Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES: S
CORRESPONDENCES: ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
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ZIP: 92030
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windiws95
SOFTWARE: FASTEM: Windiws95
SOFTWARE: FASTEM: Windiws95
SOFTWARE: FASTEM: Windiws95
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1262; DB 10;
Pred. No. 1.4e-117;
1; Mismatches 2;
                                                                                            US-00-967-301-2

Sequence 2, Application US/09967301

Publication No. US20030175859A1

Publication No. US20030175859A1

APPLICANT: Stubbe, Simon L.

APPLICANT: Jones, Anne E.

APPLICANT: Thomas, Nicholas

TITLE OF INVENTION: Pluorescent Proteins

TITLE OF INVENTION: Pluorescent Proteins

TITLE OF INVENTION: Pluorescent Proteins

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: GB 0109858.1

PRIOR APPLICATION NUMBER: GB 0109858.1

PRIOR PILING DATE: 2001-04-23

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 238
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; Sequence 2, Application US/10057505
; Publication No. US20020164674A1
; GENERAL INFORMATION:
    APPLICANT: HER REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: AURORA BIOSCIENCES CORPORATION
; APPLICANT: TSIEN, ROGER
; APPLICANT: TSIEN, ROGER
; APPLICANT: CUBITY, Andrew
; TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
; FILE REFERENCE: REGEN1260-3
; CURRENT APPLICATION NUMBER: US/10/057,505
; CURRENT PILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/396,003
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2:
    LENGTH: 238
                                                                                                                                                 NAME: Haile, Liea A.

REGISTATION UNDERE: 38,347

REFERENCE/DOCKET NUMBER: 07257/032002

TELECOMMUNICATION INFORMATION:

TELEFANE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:
APPLICATION NUMBER: 08/727,452
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: U995/14692
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: 08/337,915
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECTLE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-10-057-505-2
                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.7
Matches 235; Conservative
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Score 1262; DB 13; Length 238; Pred. No. 1.4e-117;

98.94;

Query Match Best Local Similarity

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Publication No. US20030170767A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE APPLICAMT: Audrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REPERENCE: AURO1270 (08366/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/09/129,192
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SEQ ID NO S: 74
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Sequence 74, Application US/10293580
Publication No. US20030170767A1
GENERAL INFORMATION:
APPLICANT: Autoreas Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AURO1270 (08366/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/09/129,192
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                                                      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                               1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
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   1; Mismatches
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Best Local Similarity 98.7<sup>3</sup>
Matches 235; Conservative
   235; Conservative
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| TYPE: PRT
| ORGANISM: Aequorea
| US-10-293-580-2
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181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
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SEQ ID NO 2
LENGTH: 238
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US-10-724-178-2
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Best Local Similarity 98.74
Matches 235; Conservative
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US-10-293-580-74
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publication No. US2003021226541
General Develor De
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              PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.0
SEQ ID NO 74
LENGTH: 238
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US-10-457-982-2
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Sequence 2, Application US/10724178
; Sequence 2, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INPORMATION:
   APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: ECAMCEMENTATION ASSAYS
; TITLE OF INVENTION: COMPLEMENTATION ASSAYS
; TILE OF INVENTION: UMBER: US/10/724,178
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT APPLICATION NUMBER: US 60/461,133
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
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US-10-668-168-2

Sequence 2, Application US/10668168

Sequence 2, Application US/10668168

Bublication No. US20040086968A1

GENERAL INFORMATION:
MALTE OF INVENTION:
TITLE OF INVENTION:
MALTE OF INVENTION:
CURRENT FILE REFERENCE: 0942-4020002

CURRENT FILING DATE: 1994-12-23

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 09/970,762

PRIOR FILING DATE: 1997-11-14

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATCHING DAY: 1206-11-15

NUMBER OF SEQ ID NOS: 17
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US-10-668-168-2
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Pred. No. 1.4e-117;
Length 238;
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 98.9%; Score 1262; DB 16; 98.7%; Pred. No. 1.4e-117; ive 1; Mismatches 2;
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US-10-757-624-2
i Sequence 2, Application US/10757624
j Publication No. US20040138420A1
GENERAL INFORMATION:
i APPLICANT: Stubbs, Simon L. J.
j APPLICANT: Jones, Anne E.
j APPLICANT: Michael, Nigel P.
j CURRENT FILORES: PA0111
CURRENT APPLICATION NUMBER: US/10/757,624
CURRENT APPLICATION NUMBER: US 09/967,301
j PRIOR FILING DATE: 2001-09-28
j SOFTWARE: PatentIn version 3.2
j SEQ ID NO 2:
j SEQ ID NO 3:
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US-10-505-486-3
'Sequence 3, Application US/10505486
'Publication No. US20050118639A1
'GENERAL INFORMATION:
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US-10-757-624-2
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Best Local Similarity 98.7
Matches 235; Conservative
   Query Match
Best Local Similarity 98.7
Matches 235; Conservative
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98.7%; Pred. No. 1.4e-117;
tive 1; Mismatches 2;
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: POS. 0006FQT
CURRENT APPLICATION NUMBER: US/10/505,486
CURRENT FILING DATE: 2004-08-20
FRIOR APPLICATION NUMBER: JP 2002-45728
FRIOR APPLICATION NUMBER: JP 2002-45728
FRIOR PILING DATE: 2002-02-22
FRIOR APPLICATION NUMBER: JP 2002-213949
FRIOR FILING DATE: 2002-07-23
FRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
SEQ ID NOS: 233
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Job time : 114 secs
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ORGANISM: Aequorea coerulescens
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Best Local Similarity 98.7
Matches 235; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 16, 2005, 17:06:47 Run on:

7; Search time 24.5 Seconds (without alignments) 934.677 Million cell updates/sec

US-10-757-624-4 1276 1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Title: Perfect score:

Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: piri: \* 2: piri: \* 3: piri: \* 4: pir4: \* \*:64 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ū	Description
1	1252	98.1	238	-	J01514	green-fluorescent
1 (4)	100	7.8	785	7	H72228	hypothetical prote
m	98.5	7.7	887	~	E82590	
4	92.5	7.2	534	-	NICIMA	nitrogenase (EC 1.
ß	92	7.2	336	~	C64468	hypothetical prote
ø	91	7.1	439	~	JH0414	synaptogamin o-p65
7	89	7.0	1224	-	ERHUAH	coatomer complex a
80	88.5	6.9	861	~	H64102	leucine-tRNA ligas
O	88	6.9	531	~	C95338	-
10	87.5	6.9	370	~	E70390	iron-sulfur cofact
11	87	6.9	357	~	G81355	tRNA (uracil-5-)-m
12	86.5	6.9	2222	Н	A36028	DNA-directed DNA p
13	86.5	6.8	2573	~	D71614	hypothetical prote
14		6.7	281	~	AD2052	
15	85.5	6.7	263	7	S53488	water-stress-induc
16	'n	6.7	700	-	CIHUH2	calpain (EC 3.4.22
17	ഹ	6.7	797	~	JC4078	protective surface
18	85.5	6.7	808	~	F64102	protective surface
19	ഗ	6.7	860	~	AC0582	leucyl-tRNA synthe
20	85	6.7	471	7	T27856	hypothetical prote
21	85	6.7	632	~	T06586	DNA-binding protei
22	84.5	9.9	564	~	E81317	ABC-type transport
23	84.5	9.9	655	~	D83917	DNA topoisomerase
24	84.5	_	889	~	JC5576	inter-alpha-trypsi
25	83.5	Ī	422	~	B24815	calpain (EC 3.4.22
26	82.5	6.5	312	~	C81710	thioredoxin reduct
27	82.5	_	1134	~	A60234	IgA Fc receptor pr
28	82.5	6.5	1164	-	FCSOAG	IgA Fc receptor pr
53	82	6.4	470	0	T31049	hypothetical prote

hypothetical prote oligoendopeptidase hypothetical prote DNA-directed DNA p polyketide synthas synaptotagmin II - hypothetical prote S-layer protein propothetical protein propototein conserved hypothetic proprotein convert proprotein convert proprotein convert proprotein convert proprotein convert proprotein convert diagrams of the convert proprotein convert diagrams of the convert diagr	dihydrolipoamide d probable oxysterol hypothetical prote
C90208 A99552 C70031 A12140 BWRT2Y BWRT2Y BWRT2Y G84245 C64613 KKRTC1 AB1055	E84715 T25012
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	4 4 4 4 2 6 4 3

### ALIGNMENTS

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H	4
į	F

green-fluorescent protein [validated] - hydromedusa (Aequorea victoria)

C;Species: Aequorea victoria C;Species: 03-Dec-1999 #text\_change 09-Jul-2004 C;Accession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331 R;Prasher, D.C.; Bckenrode, V.K.; Ward, W.W.; Prendergast, P.G.; Cormier, M.J. Gene 111, 229-233, 1992 A;Title: Primary structure of the Aequorea victoria green-fluorescent protein. A;Reference number: JQ1514; MUID:92175527; PMID:1347277

A;Molecule type: DNA Rheaiduea: 1-107, 'S',109-238 <PRA1> A;Gross=references: UNIFROT: F42212; UNIPROT:Q17106; UNIPROT:Q17105; GB:M62654; NID:g1556 A;Accession: JQ1514

A;Molecule type: mRNA A;Residues: 1-99, F', 101-140, L', 142-218, 'V', 220-238 <PRA2> A;Cross-references: GB:M62653; NID:9155660; PIDN:AAA27721:1; PID:9155661 A;Accession: PQ0335

A,Molecule type: protein
A,Molecule type: protein
A,Redidues: 46-64;74-12;132-151;154-183;185-200 <PRA3>
R,Incuye, S.; Teuji, F-12;
FBBS Lett. 351, 211-214, 1994
A,Title: Widence for redox forms of the Aequorea green fluorescent protein.
A,Reference number: 848693; MUID:94364470; PMID:8082767
A,Recession: \$48693

A,Status: preliminary
A,Actous: preliminary
A,Actous: preliminary
A,Robelucus: 1-24, 0', 26-156, P',158-171, K',173-238 <INO>
A,Rosidues: 1-24, 0', 26-156, P',158-171, K',173-238 <INO>
A,Cross-references: GB:L29345; NID:g606383; PIDN:AAA58246.1; PID:g606384
A,Ratkins, J.N.; Campbell, A.K.
submittins, J.N.; Campbell, A.K.
A,Reference number: S51330

A; Accession: S51330

A;Molecule type: mRNA A;Residues: 1-13.7V',15-24,'Q',26-44,'N',46-153,'G',155-156,'P',158-171,'K',173-227,'R', A;Crose-references: EMBL:X83959; NID:gG34008; PIDN:CAA58789.1; PID:gG34009 A;Experimental source: clone gfpl

A; Accession: S5131
A; Accession: S5131
A; Accession: S5131
A; Accession: S5131
A; Molecule type: mRNA
A; Molecule to the Molecule to the Molecule type: Molecule to the Brookhaven Protein Data Bank, August 1996
A; Reference number: A6562; PDB: 1GFL
A; Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A', 2-79, 'R', 81-5
A; Note: engineered sequence based on J01514, cloned and expressed in Escherichia coli
B; Yang, F; Moss, L.G.; Phillips Jr., G.N.
A; Wardy F: Moss, L.G.; Phillips Jr., G.N.
A; Title: The molecular structure of green fluorescent protein.
A; Reference number: A58953; MUID: 98294543; PMID: 9631087

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A; Contents: annotation
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                                                  leucyl-tRNA
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A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H7228
A;Actession: H7228
A;Actession: Dreliminary
A;Molecule type: DNA
A;Residues: 1-785 <ARNA
A;Residues: 1-785 <ARNA
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H7228
hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
C;Species Thermotoga maritima
C;Species 11-Un-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: H7228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
A; Contents: annotation; X-ray crystallography, 1.9 angstroms
C; Comment: This protein is excited by the photoprotein aequorin (see PIR:AQJFNV) emittin C; Comment: The chromophore of this protein is formed by modification of Ser-Gehydro-Tyr-C; Genetics:
G; Genetics:
A; GFP
A; Introns: 69/3; 167/3
C; Superfamily: green-fluorescent protein
C; Superfamily: green-fluorescent protein
F; 65-67/Cross-link: 5-imidazolinone (Ser-Gly) #status experimental
F; 66/Modified site: dehydrotyrosine (Tyr) #status experimental
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                                                                                                                                                                                               Length 238;
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                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                              Score 1252; DB 1;
Pred. No. 3.1e-99;
5; Mismatches 2;
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Best Local Similarity 97.1%;
Matches 231; Conservative :
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synthetase XF2176 [imported] - Xylella fastidiosa (strain 9a5c)
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23.2%; Pred. No. 2.8;
tive 27; Mismatches 68;
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C;Superfamily: leucine-tRNA ligase
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Best Local Similarity 23.2*
Matches 46; Conservative
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"itrogenase (EC 1.18,6.1) molybdenum-iron protein alpha chain [validated] - Clostridium introgenase alpha chain; nitrogenase component I alpha chain NiAlternate names: dinitrogenase alpha chain; nitrogenase component I alpha chain C; Species: Clostridium pasteurianum C; Spaces S

A;Molecule type: DNA A;Reaidues: 1-534 <WAN> A;Cross-references: UNIPROT:P00467; EMBL:Y00155; NID:g40583; PIDN:CAA68349.1; PID:g580995 R;Chen, K.C.

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---KDAHNDDLLNEILDYYVLKEFI 332
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A;Map position: FOR1295121-1296131
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A;Residues: 1-439 <WEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 2-41, K', 43-94, 'D', 96-180 <HAS>
B;Kim, J.; Woo, D.; Rees, D.C.
Bubmitted to the Brookhaven Protein Data Bank, March 1993
A;Reference number: A51301; PDB:1MIO
A;Reference number: A51301; PDB:1MIO
A;Reference number: A51301; PDB:1MIO
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 2-425,'A',427-526
C;Comment: The key enzymatic reactions in nitrogen fixation are catalyzed by the nitrogen did the iron protein (also called component II or nitrogense reductase).
C;Comment: Bach alpha/beta dimer covalently binds one molybdenum-iron-sulfur cluster and C;Genetics:
J. Bacteriol. 166, 162-172, 1986

A, Title: Structural features of multiple nifH-like sequences and very biased codon usage A, Reference number: 140814; MUID:86168010; PMID:3457003

A, Reference number: 140816

A, Rolecule type: DNA

A, Molecule type: DNA

A, Residues: 1-167 < CHE>

A, Rose-references: GB:M21537; NID:g144870; PIDN:AAA83531.1; PID:g551775

R, Hase T.; Nakano, T.; Matsubara, H.; Zumft, W.G.

J. Blochem. 90, 295-298, 1981

A, Title: Correspondence of the larger subunit of the MoFe-protein in clostridial nitroge A, Recession: A00545; MUID:82030699; PMID:7026551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Start codon: GTG
C;Complex: heterotetramer of two alpha and two beta chains
C;Complex: heterotetramer of two alpha and two beta chains
C;Complex: heterotetramer of two alpha and two beta chains
C;Complex: heterotetramer complex catalyzes the reduction of dinitrogen to 2 molecules c
A;Puthway: nitrogen fixation
C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain
C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain #status experimental c
F;2-534/Product: nitrogenase wanadium-iron protein alpha chain homology cVIA>
F;5-522/Domain: nitrogenase vanadium-iron protein alpha chain homology cVIA>
F;5-524/Pinding site: 4Fe-4S cluster 1 (Cys) (covalent) #status experimental
F;79/Binding site: homocitryl Mo-7Fe-8S cluster (Cys) (covalent) #status experimental
F;482/Binding site: homocitryl Mo-7Fe-8S cluster molybdenum (His) (ligand) #status exper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G6468

C9468

C) Protherical protein MJ1348 - Methanococcus jannaschii

C) Species: Machanococcus jannaschii

C) Pate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C) Accession: C64468

S; Rall, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

Reich, C.J.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 -----PILVITILIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNY-KTRA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVK------FEGDTLVNRIELKGIDFKEDGNILGHKLEY--------NYNSH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : | : | : | 335 QGKTACLYVGGSRSHTYMMMLKSFGVDSLVAGFEFAHRDDYEGREVIPTIKIDADSKNIP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 NVYIMADKOKNGIKVNFKIRHNIEDGGVOLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMDRVLEKIGYHVNATLIGDATYEKVQNADKADLNLVQCHRSINYIAEMMETKYGIPWIK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 CNFIGVDGIVETLRDMAKCFDD-PELTKR-----TEBVIAEBIAAIQDDLDYFKBKL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: |:| :: | :: | :: | :: | : | : : | : | : : | : | :: | : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 92.5; DB 1; Length 534;
19.9%; Pred. No. 4.7;
tive 39; Mismatches 97; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K 455
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A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64468
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q58743; GB:U67574; GB:L77117; NID:g1591978; PIDN:AAB99360.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P24506; GB:M64276; NID:9213110; PIDN:AAA49228.1; PID:9213111
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A;Residues: 'MLV'.26-34;'XX',194-199,'X',201-206;'X',322-332,'D',334-337 <WEN1>
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Keywords: glycoprotein; membrane protein; synaptic vesicle
F;75-101/Domain: hydrophobic <HYD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 MLFKEYFDLDBFNEIEKNKINLIVDIAYNLKNGNVKKEBWLNRINEIYKEIIKRPLPNTY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synaptogamin o-p65-B - electric ray (Discopyge ommata)
N;Alternate names: synaptic vesicle protein o-p65-B
C;Species: Discopyge ommata
C;Species: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
C;Accession: JH0414; PS0223
R;Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.
Neuron 6, 993-1007, 1991
A;Fitle: Differential expression of the p65 gene family.
A;Reference number: JH0413; MUID:91273991; PMID:2054189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VITLIYGV-----QCFSRYPDHMKR------HDFFKSAMPEGYVQERIIFFKDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPV-PWPTLVTTLTYGV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 92; DB 2
Best Local Similarity 24.9%; Pred. No. 2.8;
Matches 66; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
Total Similarity 20.1%; Pred. No. 4.9;
Pses 58; Conservative 44; Mismatches
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Nationary Leads (Strain Rd KW20)
Nationary Light Synthetase
Nationary Law Synthetase
Nationary Law Synthetase
C;Species: Haemophilus influenzae revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64102
R;Pleischmann, R.D; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I; Glodek, A.; Kirkness, E.F.; Kerlavage, A.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J., Aritle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Accession: 
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A; Residues: 1-531 «KUR»
A; Rolecule type: DNA
A; Residues: 1-531 «KUR»
A; Rolecule type: DNA
A; Residues: 1-531 «KUR»
A; Cross-references: UNIPROT: Q92Z81; GB: AE006469; PIDN: AAK65269.1; PID: g14523721; GSPDB: GR
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Cahin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authoris: Kahin, D.; Kahin, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Cl
A; Aftle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
A; Contents: annotation
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 TGDKLPI-WVANFVLMHYGTGAVMAVPAHDORD--FEFACKYSLPIKQVIAPLADEEIDL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 YRLRDWGVSRQRYWGAPIPMLTLENGDVVPA------PMEDLPILLPEDVWMDGVKSPI 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 RAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADK-QKNGI---KVN 164
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C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 6.9%; Score 88.5; DB 2; Length 8 Local Similarity 24.3%; Pred. No. 19; es 45; Conservative 26; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 FKIRH----
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468 NADPN 472
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Best Local Si
Matches 45;
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NiAlternate names: HBP-COP; xenopein homolog; xenopein-related peptide precursor
NiContains: xenin 35; xenopein-related peptide
Costoner and the manes: HBP-COP; xenopein homolog; xenopein-related peptide
Costoner and the man 
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                                                                                                                                   ---KNDINMK---DVKGSGGNQDDD 138
                                                                                                                                                                                                                                                          -NVYIMADKQKN-GIKVN------FKIRHNIEDGGVQLA-----DHYQQNTP 187
                                                                                                                                                                                                                                                                                                                     689 IVEMCYQRIKUFDKVSFLYLITGNLEKLRKMMKIABIRKDMSGHYQNALYLGD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGDGPVLLPD-----NHYLSTQSALSKDPNEKRDHMVLLEFVTAAG 228
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                                                                                      ---DILVNRIELKGIDFKEDGNI--LGHKLEYNYNSH-----
97 CLCICKKCCCKKKKNKKEKGKGK-
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41; Conservative 2
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: Gal355
C;Accession: Gal355
C;Accession: Gal355
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chillin. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel. Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-37. <PAR>
A;Cross-references: UNIPROT:Q9PP92; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7309
A;Experimental source: serotype O2, strain NCTC 11168
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C; Species: Saccharomyces cerevisiae
C; Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: A36028; B36028; S65019; S63235; S65121
R; Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Cell 62, 1143-1151, 1990
A; Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A; Reference number: A36028; MUID: 90381771; PMID: 2169349
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A;Cross-references: EMBL:271538; NID:g1302316; PIDN:CAA96169.1; PID:g1302317; GSPDB:GN00
A;Experimental source: strain S288C
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A;Residues: 1.-222 <MOR>
A;Cross-references: UNIPROT:P21951; GB:M60416; GB:M36724; NID:g171408; PIDN:AAA88711.1;
A;Accession: B36028
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A; Readues: 1324-1312, xx, 1218-1221 <MO2>
A; Readues: 1324-1312, xx, 1218-1221 <MO2>
A; Readues: 1324-1312, xx, Eleig, U.; Miedenthal, R.N.; Hegemann, J.M.
Bubmitted to the EMBL Data Library, October 1995
A; Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV
A; Reference number: $60909
A; A; Reference number: $60919
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A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996
A;Reference number: 863235
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C;Keywords: methyltransferase; S-adenosylmethionine
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24.8%; Pred. No. 8.2;
[ve. 18; Mismatches
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Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 ERSPSISSVIMPKFFGABIVNKLSEKGIYCSTGSACLSGEYEPNKHMLKMGFSQEKALRM 342
                                                                                                                                                                                                                                                                                                               ------LQF---DAKAPSGWDYVICES 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 TYGNIEREEADDAARRHILRSEVLTAAHPNGALLIPSFAVERTOELLTDLVHLMETGAVP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IKVN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LPDNHYL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 BLFTGVVPILVBLDGDVN-GHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTL
                                                                                                                                                                                                                                                                                                                                                                                         TYGVQCFSRYPDHMKRH----DPPKSAMPEG-----YVQERT-----IPFKD----
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                                                                                                                                                                          87; Indels 122;
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                                                                                                   Length 531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DGNITGHKLE-YNYNSHNVYIMADKQKNG-
                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 87.5; Dilarity 25.4%; Pred. No. 7.8; Conservative 30; Mismatches
                                                                                                6.9%; Score 88; DB 20.4%; Pred. No. 11; ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                   EIGTGPSPLRLLFSGDIGPRHKL--
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                                                                                                                                     Local Similarity 20.49
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Matches 49; Conserv
A;Gene: SMal131
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                   176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
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                                                                                                       Query Match
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C; Accession: AD2052
R; Kaneko, T.; Nakamu
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Dyleid

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Dypotherical protein PFB0460c - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Species: Plasmodium falciparum

C;Species: Dyleid

G;Accession: Dyleid

G;Accession: Dyleid

G;Accession: Dyleid

G;Accession: Dyleid

G;Accession: Dyleid

A; Pertea, M.; Salzberg, S; Zhou, L.; Sutton, G.G; Clayton, R.; White, O.; Smith, H.O.

Science 282, 1126-1132, 1998

A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A;Reference number: A71600; MUD:99021743; PMID:9804551

A;Accession: Dyleid

A;Ression: Dyleid

A;Ression: Dyleid

A;Ressiones: 1-2573 «GAR»
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A;Experimental source: clone 3D7
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from A;Reference number: S65121; MUID:96310631; PMID:8740425
A;Actersion nucleic acid sequence not shown; translation not shown A;Relevance Lype: DNA
A;Restdues: L-2221 casts
A;Restdues: L-2221 casts
A;Cross-references: EMBL:X92494; NID:91045236; PIDN:CAA63235.1; PID:91045247
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 LPVPWP-TLVTTLTYGVQCFSRYPDHM-----KRHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                     C,Genetics:
A,Gene: SGD:POL2; DUN2; MIPS:YNL262w
A,Cross-references: SGD:S0005206; MIPS:YNL262w
A,Map position: 14L
C,Superfamily: DNA-directed DNA polymerase II
C,Superfamily: DNA-directed DNA polymerase; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
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6.8%; Score 86.5; DB 2;
Best Local Similarity 26.2%; Pred. No. 1.2e+02;
Matches 34; Conservative 29; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.8%; Score 86.5; D
Best Local Similarity 28.2%; Pred. No. 98;
Matches 37; Conservative 14; Mismatches
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TYLKRERDYM 246
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A,Gene: PFB0460c
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RESULT 14 AD2052

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Vincessium, nazura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A.Res. 8, 205-213, 2001

A.Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Reference number: AB1807; MUD:21595285; PMID:11759840

A.Recession. AD2052

A.Status: preliminary
A.Molecule type: DNA
A.Residuus: 1-281 **CUR>
A.Residuus: 1-281 **CUR>
A.Residuus: VCUR>
A.Residuus: VCUR>
A.Residuus: VCUR>
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A.Residuus: Complete Comple
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C;Species: Solanum chaccense (Chaco potato)
C;Accession: S53488
R;Silhavy, D.; Hutvagner, G.; Barta, E.; Banfalvi, Z.
Plant Mol. Biol. 27, S87-595, 1995
A;Tile: Isolation and characterization of a water-stress-inducible cDNA clone from Solarian and characterization of a water-stress-inducible cDNA clone from Solaria, Reference number: S53488
A;Reference number: S53488
A;Reference number: S53488
A;Reference number: S53488
A;Reference number: S53488
A;Residues: 1-263 < SIL>
A;Residues: 1-263 < SIL>
A;Residues: 1-263 < SIL>
A;Cross-references: UNIPROT:Q41300; GB:U12439; NID:g607904; PIDN:AAA86052.1; PID:g607905
hypothetical protein all1970 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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Best Local Similarity 24.4%; Pred. No. 7.3;
Matches 33; Conservative 26; Mismatches 54; Indels
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Best Local Similarity 22.3%; Pred. No. 7.4;
Matches 46; Conservative 21; Mismatches 88;
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(c) 1993 - 2005 Compugen Ltd
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2: uniprot_trembl:*
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## ALIGNMENTS

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Bacteria, Proteobacteria, Gamm
Pseudomonadaceae, Azotobacter.
NCBI_TaxID=354;
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AC P42Z12; Q17104; Q27903;
                                                                              PRELIMINARY;
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MEDLINE=97299833; PubMed=9154981; DOI=10.1023/A:1005740823703; Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.; Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage."; Plant Mol. Biol. 33:989-999(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION. MEDLINE=98455509; PubMed=9782051; DOI=10.1016/S0969-2126(98)00127-0; Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein."; Structure 6:1267-1277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-99238303; PubMed-10220315; DOI=10.1021/bi9902182;
Elsilger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
"Structural and spectral response of green fluorescent protein
"Structural and spectral response of green fluorescent protein
variants to changes in pl.";
Biochemistry 38:5296-5301(1999).
-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the
blue chemiluminescence of the protein aequorin into green
fluorescent light by energy transfer. Fluoresces in vivo upon
receiving energy from the Ca(2+)-activated photoprotein aequorin.
Absorbs light maximally as 1395 nm and exhibits a smaller
absorbance peak at 470 nm. The fluorescence emission spectrum
peaks at 509 nm with a shoulder at 540 nm.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94185810; PubMed=8137953; DOI=10.1016/0014-5793(94)80472-9;
Inouye S., Tsuji F.I.;
"Aequorea green fluorescent protein. Expression of the gene and fluorescence characteristics of the recombinant protein.";
FEBS Lett. 341:277-280(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cody C.W., Prasher D.C., Westler W.M., Prendergast F.G., Ward W.W.; "Chemical structure of the hexapeptide chromophore of the Aequorea
                                                                                                                                                                                                                  MEDLINE-92175527; PubMed-1347277; DOI-10.1016/0378-1119(92)90691-H; Pranher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G., Cormier M.J.;
                                                                                                   Aequorea victoria (Jellyfish).
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
                                                                                                                                                                                                                                                                                   'Primary structure of the Aequorea victoria green-fluorescent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96355665; PubMed-8703075;
Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98294543; PubMed=9631087;
Yang F., Moss L.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Biotechnol. 14:1246-1251(1996).
  (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 45, Last annotation update)
                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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Biochemistry 32:1212-1218(1993).
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                                                           Green fluorescent protein.
                                                                                                                                     Aequoreidae; Aequorea.
NCBI_TaxID=6100;
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01-NOV-1995 (Rel.
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25-OCT-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              of modified amino acid residues. The chromophore, which is composed of modified amino acid residues. The chromophore is formed upon cyclization of the residues Ser-dehydroTyr-Gly.

-I- BIOTECHNOLOGY: Has become a useful and ubjquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein tag. GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, prosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in laving cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

-I- DATABASE: NAME=Protein Spotlight, NOTE=Issue 11 of June 2001, WWW="http://www.expasy.org/spotlight/articles/sptlt011.html".
-!- SUBUNIT: Monomer.
-!- TISSUE SPECIFICITY: Photocytes.
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@=1-238.
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A/B/C=1-238.
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EMBL; M62653; AAA27721.1; -.
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1C4F; X-ray; A=1-238.
1CV7; X-ray; A=1-228.
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2EMO;
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NCBI_TaxID=116849;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacese; Azotobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Koranyi P., Berenyi M., Burg K.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR34407; AAN86139.1; -.
HSSP; P42212; 1BSC.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_IAke.
InterPro; IPR001786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
PRINTS; PR01229; GFLUORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26886 MW; EA5A6F2IFBFB6E05 CRC64;
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Koubali (MOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF3340405; AAN86137.1; -1.
HSSP; P42212; 1BFP.
GO; CO0066091; P:energy pathways; 1EA.
InterPro; IPR011584; GFP_related.
InterPro; IPR010786; Green_fl_protein.
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescence protein.
                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                               Created)
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                                                                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Green fluorescence protein. Name=289Gfp;
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Matches 234; Conservative
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Q71RY9,
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InterPro; IPR009017; GPP_like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GPP; 1.
PRINTS; PR01229; GFL00RESCENT.
Propom; PD013756; Green_fl_protein; 1.
3D-structure; Direct protein sequencing; Luminescence.
CROSSLNK 65 67 5-imidazolinone (Ser-Gly).
MOD RRS 66 66 (Z)-2,3-didehydrotyrosine.
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98.3%; Pred. No. 3.4e-93;
tive 1; Mismatches 3; Indels
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Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFL00RESCENT.
ProDom; P0013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE989C5B4F6B89 CRC64;
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238 AA; 26887 WW; E0E1616BD2AF6188 CRC64;
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                                                                                                Score 1257; DB 2;
Pred. No. 2.8e-93;
1; Mismatches 3;
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Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Azotobacter.
NCBI_TaxID=354;
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PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Yeast-enhanced green fluorescent protein (yEGFP)a reporter of gene expression in Candida albicans.";
Microbiology 143:303-311(1997).
EMBL; U73901; AAB18957.1; -.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96305137; PubMed=8707053; DOI=10.1016/0378-1119(95)00685-0;
COTMENCE B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
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Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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Aeguoreidae; Aeguorea.
NCBI_TaxID=6100;
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Cormack B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
10-CT-2003 (TEMBLrel. 25, Last annotation update)
Green fluorescent protein mutant 3.
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98.1%; Score 1252; DB 2; 1
Best Local Similarity 97.9%; Pred. No. 7.1e-93;
Matches 233; Conservative 2; Mismatches 3;
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238
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GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR011584; GFP_related.
InterPro; IPR007086; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
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PRT;
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  PRELIMINARY;
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                                                                                                                                                             Name=GFP;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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Best Local Similarity
Matches 217; Conserv
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Qeygzo;
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Q8WTC6
ID Q8WTC
AC Q8WTC
DT 01-MAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238
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Aequoreidae, Aequorea
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95.3%; Score 1216; DB 2; Length 238;
Best Local Similarity 94.1%; Pred. No. 5.6e-90;
Matches 224; Conservative 7; Mismatches 7; Indels (
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            SEQUENCE FROM N.A.
Watkins J.N., Campbell A.K.;
Submitted (UAN-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (UAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83959; CAN58789-1; -.
PIR, J80692; JQ1514.
HSSP; P42212; IGFL.
GO, GO:0006091; Perenergy pathways; IEA.
InterPro; IPR0109017; GFP like.
InterPro; IPR011584; GFP related.
InterPro; IPR011584; GFP related.
InterPro; IPR011584; GFP related.
InterPro; IPR011594; GFP related.
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Watking J.N., Cambell A.K.;

Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; X83960; CAAS8790.1; -.

PIR; JS0692; JGJ114.

HSSP; P42212; 1BFP.

GO; GO:006091; Fenergy pathways; IEA.

InterPro; IPR019017; GFP_Ike.

InterPro; IPR019017; GFP_related.

InterPro; IPR01968; Green_fl_protein.

Pfam; PF01353; GFP; 1.

PRINTS; PR01229; GFLUORESCENT.

NON TER 238 A3, 2867 MW; BD4648262D8EABD4 CRC64;
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                                                                                                                                                                                                                                                                                                                                     238 AA; 26950 MW; 26E2BE450E748E44 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
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94.1%; Score 1201; DB 2;
Best Local Similarity 93.3%; Pred. No. 9e-89;
Matches 222; Conservative 8; Mismatches 8;
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SEQUENCE FROM N.A.
MEDLINE=22726112; PubMed=12693991; DOI=10.1042/BJ20021966;
MEDLINE=22726112; PubMed=12693991; DOI=10.1042/BJ20021966;
Gurekaya N.G., Fradkov A.F., Pounkova N.I., Staroverov D.B.,
Bulina M.E., Yanushevtch Y.G., Labas Y.A., Lukyanov S., Lukyanov K.A.;
R., Colourless green fluorescent protein homologue from the non-
fluorescent hydromedusa Aequorea coerulescens and its fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
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VITLIYGVQCPSRYPDHMKRHDPPKSAMPEGYVQBRIIPPKDDGNYKTRAEVKPEGDTLV
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Rukaryota; Metazos; Cnidaria; Hydrozoa; Hydroida; Leptomedusse;
Acquoreidae; Acquores.
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EMEL; AY151052; AAN41637.1; --
EMEL; AY151052; AAN41637.1; --
HSSP; PA2121; 189C.
GO; GO:006091; P:energy pathways; IEA.
Interpro; IPR01054; GPP_related.
Interpro; IPR01054; GPP_related.
Interpro; IRR00786; Green_fl_protein.
Pfam; PF01353; GPP; 1.
PRINTS; PR01229; GPLUORESCENT.
PRODOM; PD013756; Green_fl_protein; 1.
PRODOM; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26896 WW; DE72EDBB7ED9F9FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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VITLIYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,

Li S.J., Xia N.S.;

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AY013821, AAK02062.1;

EMBL, AY013821, AAK02059.1;

HSSP; P42212; 1BFP.
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                                                                   Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI TaxID=147615;
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                                                                                                                                                                                                                                                         Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B. Li S.J., Xia N.S.; Submitted (OT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF435431; AAL33916.1; -.
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Pfam; PF01353; GFP; L.
PERNYES; PR01229; GFLUORESCENT.
SEQUENCE 238 Aa; 27049 MW; 8185D0E5E529012B CRC64;
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Pfam; PF01353; GFP; II.
PRINTS; PR01229; GFLUORESCENT.
SEQUENCE 238 AA; 27015 MW; 6B8FD75E88926903 CRC64;
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Last annotation update)
Last annotation update)
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83.2%; Pred. No. 4.9e-81;
ive 20; Mismatches 20;
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; Pred. No. 2.3e-81;
20; Mismatches 19
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   01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.2
Matches 198; Conservative
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Matches 199; Conservative
                                Green fluorescent protein
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AC QUAPPS
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DT 01-MA
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                                                          NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLAD 180
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen I.Luo W.X., Zhang J.,
Luo S.J., Xia N.S.;
Submitted (OCT-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435433; AAL33918.1; -
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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86.4%; Score 1102; DB 2; Length 238;
Best Local Similarity 84.5%; Pred. No. 8.5e-81;
Matches 201; Conservative 16; Mismatches 21; Indels
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Pfam; PF01353; GFP; J.
PRINTS; PR01229; GFUJORESCENT.
SEQUENCE 238 AA; 26956 WW; 75521EAE
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Name=GFP;
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Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
Lus S.J., Xia N.S.;
EMBL, GOT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435429; AAL33914.1; -.
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              SEQUENCE FROM N.A.
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomeduaae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.2%; Score 1100; DB 2; Length 238; Best Local Similarity 83.2%; Pred. No. 1.2e-80; Matches 198; Conservative 19; Mismatches 21; Indels
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                                                                                                                    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF435427; AAL33912.1; -. HSSP; P42212; 1KYP.
                                                                                                                                                                                                                                GO; GO:0006091; P:energy pathways; IEA.
Pfam; PP01353; GFP; 1.
PRINTS; PR01229; GFLUORSCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26997 WW; 5F80A192173CB84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AA; 27047 MW; SF80A18FA1E7C84D CRC64;
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Last annotation update)
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Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                   Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 238;
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86.1%; Score 1099; DB 2; Length 2
Best Local Similarity 83.2%; Pred. No. 1.5e-80;
Matches 198; Conservative 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               (1) — SEQUENCE FROM N.A. Lin S.W., Guan B. Liu W.X., Zahang J., Yang H.J., Xie X.Y., Li S.W., Guan B. Li S.J., Xia N.S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. BMBL; AF4554218; AAL33913.1; — HSSP; P42212; IKYP. GO, GO.0006091; P:energy pathways; IEA. Penn; PF01323; GFLUORESCENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AA; 27031 MW; SF80A19C19DC584D CRC64;
                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ne : 115 secs
                                                                                                                                                                                                                                                                                         Green fluorescent protein.
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